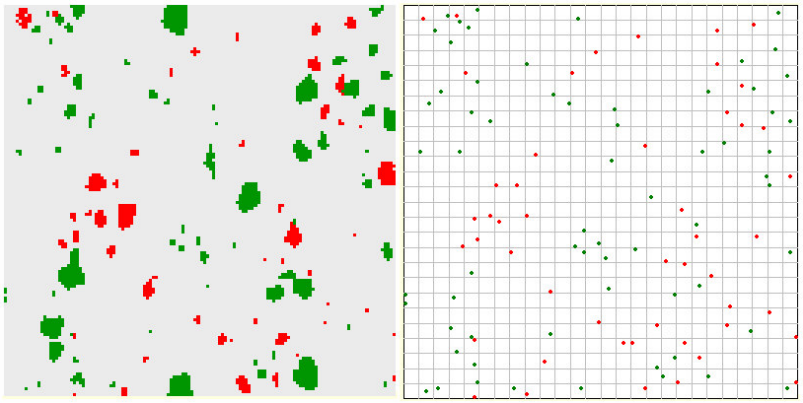
Extending Point Pattern Analysis for Objects of Finite Size and Irregular Shape using the *Programita* software

A supplementary user manual
with an collection of examples using the *Programita* software



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Programita

Abstract

The *Programita* software allows you to perform univariate and bivariate point-pattern analysis with Ripley's *L*-function, the pair-correlation function, and the *O*-ring statistic. *Programita* contains standard and non-standard procedures for most practical applications. Procedures for non-standard situations include the possibility to perform point-pattern analyses for arbitrarily shaped study regions and *Programita* offers a wide range of non-standard null models such as heterogeneous Poisson null models or cluster null models.

The grid-based implementation of *Programita* allows for a straight-forward extension of point pattern analysis to deal with objects of finite size and irregular shape (e.g., plants). The objects are approximated by using the underlying grid and may occupy several adjacent grid cells depending on their size and shape. Null models correspond to that of point pattern analysis but need to be modified to account for the finite size and irregular shape of plants.

The procedures used by *Programita* for performing analyses which consider the finite size and irregular shape of objects are described in detail in Wiegand et al. 2006. This document supplements the manual of *Programita*, focusing on analyses of objects with finite size and irregular shape.

Before starting *Programita*

Hardware requirements

Programita is a free unsupported software, developed in Borland Delphi4 under a WindowsXP environment. *Programita* is executable under 32-bit operating systems such as Windows98, Windows 2000, Windows XP or WindowsNT.

Running *Programita* requires little hard drive space. For example, for grid sizes < 200 ×200 cells *Programita* and temporally created files occupy < 10M. However, analysis of larger grid sizes may be slow for small working memory and low computer speed.

Terms of use and copyright agreement

The *Programita* software is produced by Thorsten Wiegand in his spare time. He is affiliated at the Dept. Ecological Modelling, UFZ Centre for Environmental Research Leipzig-Halle. *Programita* is intended to foster analysis of point patterns in ecology by providing ecologists a tool that contains null models and procedures not supported by most statistical packages, but which are essential for a throughout analysis of point-patterns. The *Programita* software is not a commercial venture and may be downloaded and used free of charge for purposes of scientific research and teaching. Any commercial application of the program requires the previous permission by the author. Publications must acknowledge use of the *Programita* and cite Wiegand and Moloney (2004) which describes the basic implementation and the procedures used by *Programita* and Wiegand et al. (2006) for analyses of finite size and irregular shape.

Installation

There is no setup procedure; installation of *Programita* requires only the extraction of all files from the zip file Progamita_FiniteSize.zip. Make sure that you also access the PDF (Manual_FiniteSize_Programita2006.pdf) and HTM versions (Manual_FiniteSize_Programita2006.zip) of the supplement user manual. Place the files into a directory of your choice; extracting the zip file will place all files into the sub-directory *Programita*. Note that you must place all files in the same directory; for simplicity *Programita* does not use a path variable. The zip-file contains the following files and file types:

ProgramitaJulio2006.exe	the executable of *Programita,* version 26 of July 2006
*.asc files	example data file in ArcView raster format
*.dat files	example data files and temporary files
*.int files	plug-in files for heterogeneous Poisson
*.rep files	data files to show results of previous analyses
*.res files	results and settings files

The manual of *Programita* (Manual_FiniteSize_Programita2006.pdf) and a HTM version of the manual (Manual_FiniteSize_Programita2006.zip) are provided separately. You can use the HTM version as help because it contains many textmarks and internal links for easy navigation through the document.

Screen size

Programita was designed for a screen of 1024 × 768 pixels, but it can be run as well using an 800 × 600 screen. If you execute *Programita* in the 1024 × 768 pixel mode, it must look like the segment shown in figure 1. Sometimes windows within *Programita* are truncated and one cannot see all of some buttons or headers. In this case, it is as if the window is too small to handle them. To avoid this problem, check the default letter size in the settings of your computer. Your computer may scale the letters but not the window sizes and as a consequence, the windows appear too small.

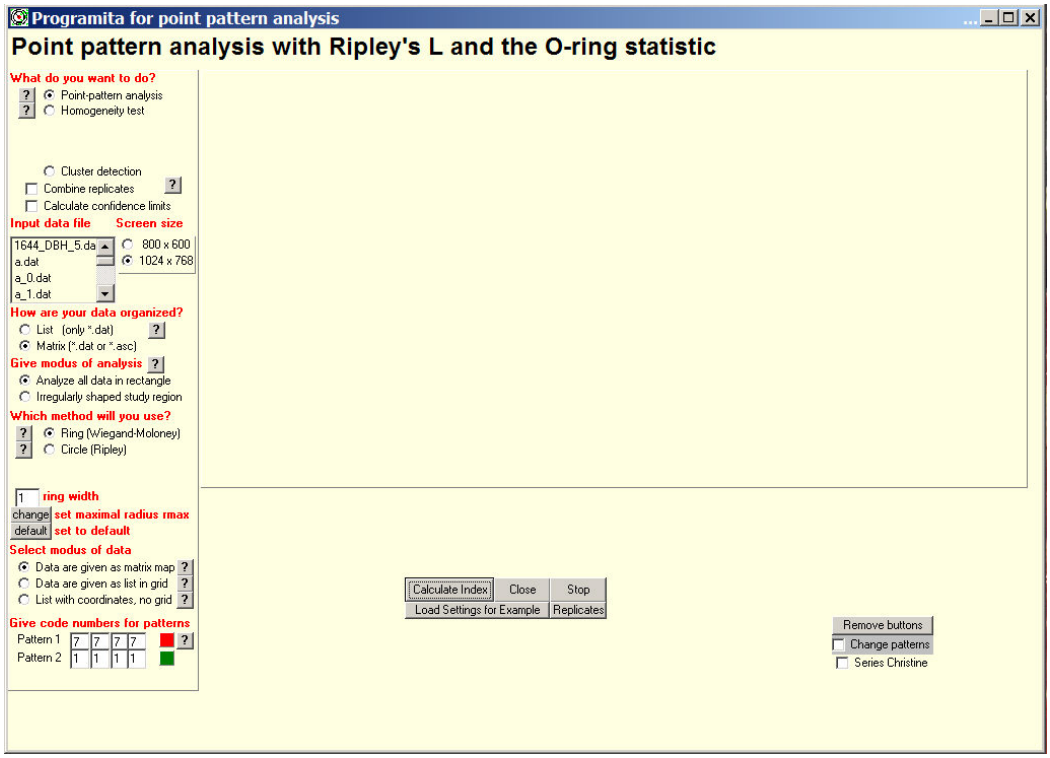


Figure 1. Correct display of the *Programita* interface under the 1024 × 768 pixel mode.

A quick start

Execute *Programita*

Execute and adjust *Programita* to your screen size. Two options are given, a screen of 800 × 600 pixels, and a larger screen of 1024 × 768 pixels which is the default.

Load a settings file to redo an analysis

There is a convenient way to quickly start with *Programita* and to learn the settings. You can read a file (a *.res-file) that contains all setting of a previous analysis and redo this analysis. For example, you can repeat all analysis show in the figures 2A - C in Wiegand et al. (2006).

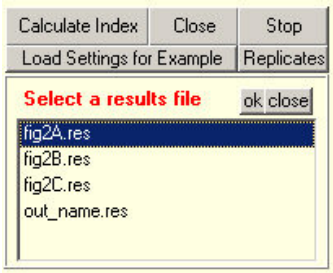


Figure 2. Load an example settings file.

To load a settings-file, apply the button “Load Settings for Example” (figure 2) and a list with files containing settings of old analysis will appear (figure 2). Select a *.res-file, for example fig2A.res, press ”ok”, and then the button “Calculate Index”. Now *Programita* performs the analysis of figure 2A in Wiegand et al. (2006).

What happens on the screen?

After loading the settings-file fig2A.res, *Programita* will automatically select all settings for the data and analysis mode and all settings for the null model that was used in the example fig2A.res.

Two plots will appear: on the left appears a plot showing the original point pattern being analyzed (figure 3a), and on the right appear the patterns of the Monte Carlo simulations of the null model used for constructing the confidence limits. After terminating the simulations of the null model, the figure with the simulated patterns of the null model disappears, and instead a figure with the result of the analysis appears on the right (figure 3b).

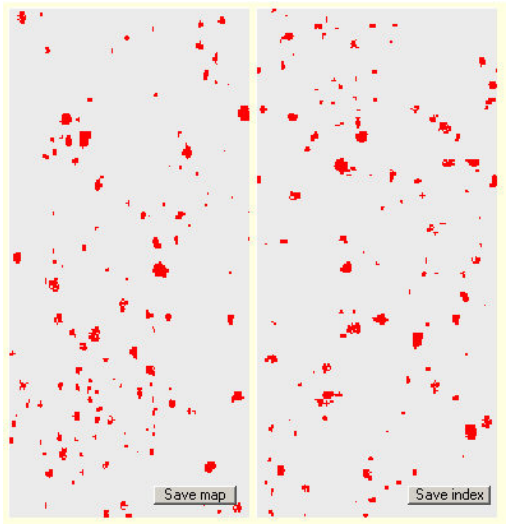
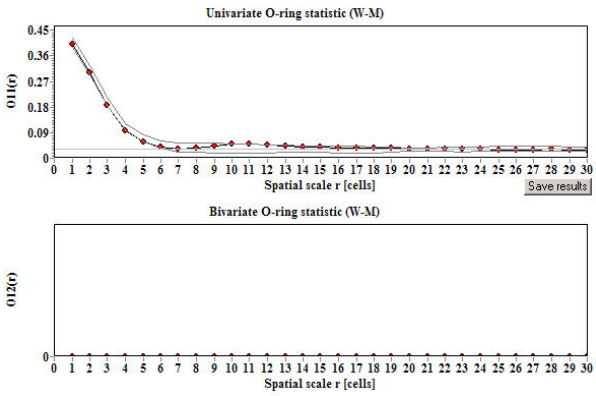
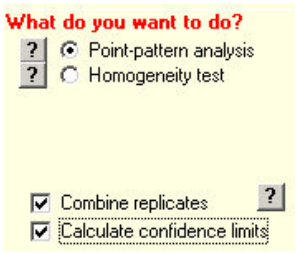


Figure 3a. Left: the point-pattern analyzed in fig2A in Wiegand et al. (2006). Right: One realization of the Monte Carlo null model that conserves the shape of the shrubs (a random pattern, CSR) used to construct the confidence limits.

Figure3b. After termination of the Monte Carlo simulations of the null model, a figure with the result appears on the right. The figure shows Wiegand-Moloney's *O*-ring statistic (or Ripley's *L*-function) together with the confidence limits for the specific null model chosen. The top figure shows the results of the univariate point pattern analysis; the bottom figure shows the results of the bivariate analysis if a second type of points was specified. In fig2A only one type of points was used. Therefore, there appears no result for the bivariate analysis.





Show results of previous analyses

Programita offers a convenient possibility to show the results of previous analyses. (This works only if the option "Combine replicates" was enabled when doing the original analysis.)

To show the results of a previous analysis, apply the button "Replicates" (figure 2) and a window with a list of results files appears (figure 4). Highlight fig.2A.rep, press "select file", and "Calculate joined statistic". The result of the analysis will appear (figure 5).

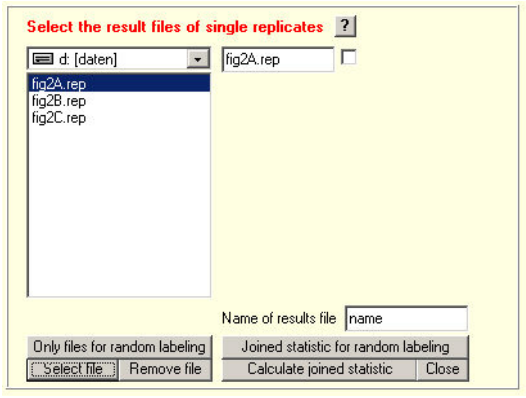


Figure 4. A list with result files which were previously saved.

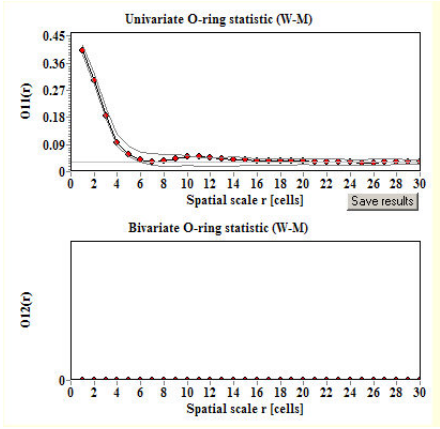


Figure 5. The results of the previous analysis fig2A.rep.

Save the results of the analysis

To save the results of the analysis, press the button “save results” that appears below the graph with the results of the univariate analysis (figure 3b), and insert a name for the result file. The results file will be saved as ASCII-file name.res in the same directory where the *.exe file of *Programita* is located. The results file (figure 6) contains the settings of this analysis and the results of the univariate and the bivariate point-pattern analysis. The results file name.res can be used (in the same way as fig2A.res) in the previous section to load the setting and to repeat the analysis.

```
Pointpattern analysis of file D:\Programita\Figure2.asc
Method Wiegand-Moloney (ring) with 99 replicates for confidence limits, ring width = 3
Test Model= 12random  1shape    *   400   400  8  smaller   4    ** 8
the null assumed homogeneous pattern(s)
Analysis modus= standard
only one point per cell allowed
All cells within the rectangle were considered for calculating the indices
number cells  of pattern 1 = 1015
number cells  of pattern 2 =    0
the rectangular area contains 130*274 = 35620   cells  (= dim1*dim2)
pattern 1 was coded with numbers 11 * 11 * 11 * 11
pattern 2 was coded with numbers 2 * 2 * 2 * 2
the mask was coded with numbers  -1 -1 -1
```

Scale	r	r	O11(r),	E11-,	E11+,	O12(r),	E12-,	E12+,
1	r	r	0.3999665	0.3856460	0.4191957	0.0000000	0.0000000	0.0000000
2	r	r	0.3003174	0.2881745	0.3228708	0.0000000	0.0000000	0.0000000
3	r	r	0.1851738	0.1748624	0.2109540	0.0000000	0.0000000	0.0000000
4	r	r	0.0968253	0.0864759	0.1244389	0.0000000	0.0000000	0.0000000
5	r	r	0.0579106	0.0485426	0.0833683	0.0000000	0.0000000	0.0000000
6	r	r	0.0391140	0.0313220	0.0652772	0.0000000	0.0000000	0.0000000
7	r	r	0.0329553	0.0220457	0.0598031	0.0000000	0.0000000	0.0000000
8	r	r	0.0361094	0.0185628	0.0582927	0.0000000	0.0000000	0.0000000
9	r	r	0.0425961	0.0186002	0.0557966	0.0000000	0.0000000	0.0000000
10	r	r	0.0484125	0.0196974	0.0514856	0.0000000	0.0000000	0.0000000

Figure 6. The *.res results file (fig2A.res). The **first lines** contain the information on the settings of the analysis; the following part contains a table with the results of the analysis. The **first column** gives the spatial scale *r* of the point-pattern analysis units of cells, the second and third column provide a summary of the Monte Carlo significance test of the null model ("-": data at scale *r* below the confidence limits, "r": inside the confidence limits, and "+": above the confidence limits; second column for univariate analysis, third column for bivariate analysis), **columns 4, 5, 6**: results of univariate analysis (column 4: univariate *O*-statistic [or *L*-function] of the data, column 5: lower confidence limit, column 6: upper confidence limit), and **columns 7, 8, 9:** results of bivariate analysis (column 7: univariate *O*-statistic or [or *L*-function] of the data, column 8: lower confidence limit, column 9: upper confidence limit).

Temporary data-files

During the analysis, *Programita* creates a number of temporary data files which are overwritten by a new analysis. Knowing these files, you may use the information they contain.

The files tempp1.dat and tempp2.dat.—The file tempp1.dat contains a matrix representation of pattern 1. The first line contains information on the dimensions of the grid: (1, number of lines, 1, number of columns). The following lines are the data matrix with the pattern. The numbers are not code numbers as in the matrix data format but give a "1" if the cell is occupied by category of pattern 1 and a "0" if the cell is not occupied by the category of pattern 1. The file tempp1.dat does not contain information on an irregularly shaped study region. The file tempp2.dat is the analogue to tempp1.dat for pattern 2.

The file temphab.dat.—If you analyze an irregularly shaped study region, *Programita* creates a matrix representation of your study region analogously to the files tempp1.dat and tempp2.dat.

The file tempp12.dat.—The file tempp12.dat is the "list in grid" representation of your data, containing the information on cells of pattern 1, pattern 2, and the study region.

The files Bi_confidence.env and Uni_confidence.env.—*Programita* uses the lowest and highest $O(r)$ [or $L(r)$] of the different simulations of the null model as default confidence limits. However, it automatically produces two temporally files (Uni_confidence.env, Bi_confidence.env) that contain the $O(r)$ [or $L(r)$] for all simulations of the null model. The columns of these files are the scales $r = 1$, r_{max}, and the lines are the different simulations of the null model. You may use this information to construct confidence limits with different definitions. Note that Programita offers the possibility to use also the 5th highest and 5th lowest $O(r)$ [or $L(r)$] out of 99 (or 999) replicate simulations of the null model for defining 95% (99%) confidence limits (e.g., Stoyan and Stoyan 1994).

The individual O and λK-function.—The individual $O(r)$ of a cell (x, y) of pattern 1 gives the density of pattern 1 cells in a ring with radius r around the focal cell (x, y). The individual $\lambda K(r)$ of a cell (x, y) of pattern 1 gives the number of pattern 1 cells in a circle with radius r around the focal cell (x, y).

The file temp_indO.dat gives the individual $O(r)$ or $\lambda K(r)$ for each point of the pattern. The file is comma-delimited and the first two columns give the x- and y-coordinates of the cell of pattern 1. The next columns give the individual univariate $O_{11}(r)$ or $\lambda K_{11}(r)$ [= O11(r) or K11(r)] for the cell (x, y) at scale r, and the individual bivariate $O_{12}(r)$ or $\lambda K_{12}(r)$ [=O12(r) or K12(r)]] for the cell (x, y) at scale r. The end of the file gives the settings file (figure 5) used to generate the data.

The files temppatch1.dat and temppatch2.dat.—These files are the "object" representation of your data of pattern 1 and pattern 2. The first line gives the number of objects of pattern 1 (or pattern 2), the next lines contain the information on the objects necessary for randomization of the objects of finite size and irregular shape.

The first two columns are the minimal x- and y- coordinates of the object, the third column gives the width of the object in x-direction (= xmax-xmin), the fourth column gives the width of the object in y-direction (= ymax-ymin), the fifth column the number of cells of the objects, and the following columns give the pairs of coordinates belonging to the object.

For example, the beginning of the temppatch1.dat is given by:

```
126
   1   185   2   2   6   1  186   1  187   2  186   2  187   2  185   3   186
```

and indicates that there are a total of 126 objects, and the minimal x- and y-coordinates of the first object are 1 and 185, respectively. The width in x- and y-direction of the object is 2 cells (xmax= 3, xmin=1; ymax=187, ymin = 185), and the object comprises the six cells (1, 186), (1, 187), (2, 186), (2, 187), (2, 185), and (3, 186).

The input data files (*.dat and *.asc data files)

Programita performs point-pattern analysis for two different situations. First, it calculates the *O*-ring statistic and the *L*-function for point patterns which are basically given as a list of points with and without a predefined grid. This corresponds to conventional point-pattern analysis.

In a second mode, *Programita* performs point-pattern analysis for categorical maps which can represent objects of finite size and irregular shape. In this case, the data input is a matrix with categories that can range from 0 to 999. In the following, we discuss the data input for categorical maps.

Because *Programita* works in the matrix mode with a category and not with number of points, the Monte Carlo simulation of null models differs slightly from the point mode. Under the mode "Matrix" the null model does not allow to have the same category two times in a given cell. However, if you enable the checkbox "Only one point per pattern" in the null-model window (figure 7), *Programita* allows having a mixed category where type 1 and type 2 are together in one cell.

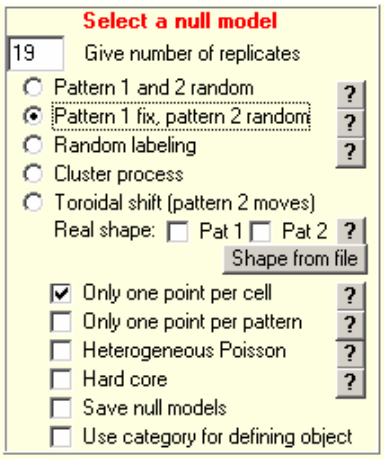


Figure 7. The null-model window for the mode "Matrix".

Preparation of data under matrix-mode

The input data are a matrix that can have the following code numbers:

- 0, 1, 2, ..., 999 if the cell is inside the study region
- -1 (or -9999) if the cell is outside the study region (mask)

Programita reads two different data formats in the matrix-mode:

1. a space (or tab) delimited ASCII-file with the *.dat extension with line breaks.
2. the ASCII format of ArcView (a ***.**asc-file) without line breaks. The head of the *.asc-file must look like this:

```
ncols 144
nrows 45
xllcorner 1
yllcorner 1
cellsize  1
nodata_value -9999
```

ncols gives the number of columns, nrows the number of rows, xllcorner the smallest x-coordinate, and yllcorner the smallest y-coordinate. The cell size must be "1" and the value for no data (the mask) must be -9999.

The matrix mode allows you to use a data matrix with different code numbers, however, calculation of Wiegand-Moloney's *O*-ring statistic and Ripley's *L*-function *Programita* requires a reduction of the original code numbers to the four categories:

- the cell is of type 1 (pattern 1)
- the cell is of type 2 (pattern 2)
- the cell is outside the study region (mask)
- the cell is empty

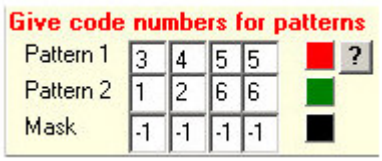


Figure 8. Transformation of the original code numbers of the data matrix to the three categories: pattern 1, pattern 2, and mask outside the study region. All other categories which are not set are automatically defined as empty cells.

If you enable the "Matrix" or "Data are given as matrix" option, the window Give code number for patterns (figure 8) appears and ask you to group your code numbers into the final categories "pattern 1", "pattern 2", and "mask". All other cells with code numbers not defines as pattern 1, pattern 2, or mask are defined automatically as empty cells. You can combine up to four code numbers (but not -1) to define "pattern 1" and "pattern 2", and up to four categories (including -1) to define the area outside the study region.

Thus, you can mask, if required, additionally cells which are part of the original study region. For example, if you study vegetation maps with category 0: bare ground, category 1: grass tufts (size of one cell) and category 2: shrubs (size of several cells) you may mask the area occupied by shrubs for studying the spatial pattern of the grass tufts. If you do not exclude the area occupied by shrubs (which cover perhaps 10% or so of the study region) a simple null model that randomizes the locations of the grass tufts (CSR) will distribute tufts at locations where they cannot occur in the field. This may introduce a bias in the analysis.

The possibility to use up to 1000 categories is a convenient feature because you can use the same data for different analyses. Be sure that a given code number does not appear in different categories. A given cell can either be pattern 1, pattern 2, empty, or mask!

Format of the *.dat matrix data file

The *.dat matrix data-file is a space (or tab) delimited ASCII-file. The first line contains information on the dimensions of the grid: (1, number of lines, 1, number of columns). The following lines are the data matrix with the different code numbers. In contrast to the ArcView ASCII matrix format, you need to insert line breaks. Note that the visualization of *Programita* corresponds to the transposed matrix. (figure 9).

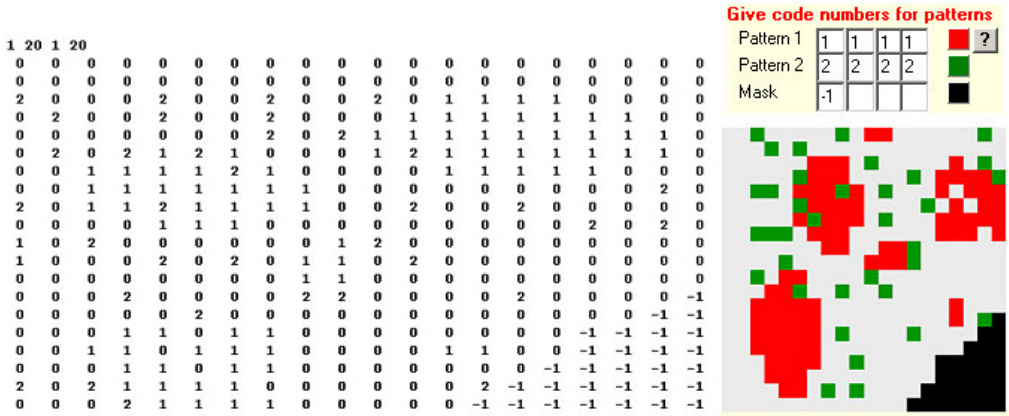


Figure 9. Example of a *.dat input data-file for the matrix mode. Shown are the file small_matrix.dat (left) and the visualization in *Programita* (right). Red: cells of pattern 1 (code 1), green: cells of pattern 2 (code 2), grey: empty cells (code 0), black: mask with cells outside the study region (code -1). The first line contains information on the grid: (1, number of lines, 1, number of columns). Note that the visualization of *Programita* corresponds to the transposed matrix.

The Settings Menu for Point Pattern Analysis

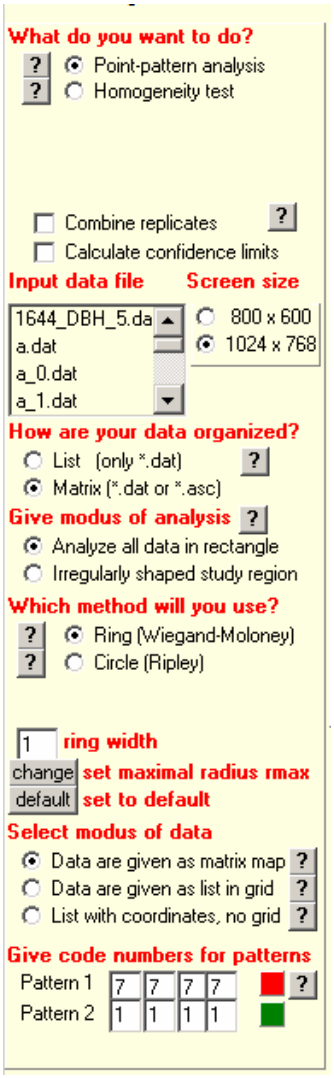


Figure 10. The settings menu for Point-pattern analysis.

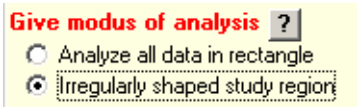
If you select in the menu What do you want to do? "Point-pattern analysis", *Programita* allows you to select different types of analysis, input data, input data formats, etc. If you do not use a *.res settings-file that stores the settings from a previous analysis you need to carefully select all settings manually from the settings menu before performing any analysis.

Programita calculates Ripley's *L* function ("Circle" in Which method will you use) and Wiegand-Moloney's *O*-ring statistic ("Ring" in Which method will you use) in a grid-based implementation for a given data-file (selected in Input data file).
In the window How are your data organized? you can select between two types of input data: (1) data which are given as a list of points and (2) categorical data which are organized as a matrix.

Matrix data

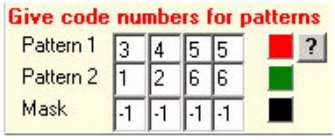
If your data are a matrix (categorical data), you need to select "Matrix" in How are your data organized?, "Data are given as matrix map" in Select modus of data, and specify in the window Give code numbers for pattern which code numbers of your data matrix make up pattern 1, pattern 2, and the mask. The mask defines the area outside the study region if your study region is irregularly shaped.

Irregularly shaped study region



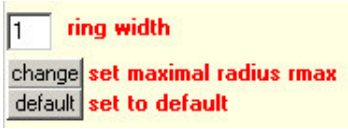
You can consider any arbitrarily shaped study region supported by the grid structure. If you select in the window **Give modus of analysis** the option "Irregularly shaped study region" some cells of the rectangular grid are not considered during the Monte Carlo simulation of the null models, and cells outside the study region are not counted for the numerical implementation of the *L*-function and the *O*-ring statistic. In contrast, if you select "Analyze all data in rectangle" the study region is the rectangle defined by your grid and all cells of the rectangle count and all cells are considered for simulation of the Monte Carlo Null models.

Irregularly shaped study region for matrix data



If your data are organized as matrix you can define a mask (cells outside the study region) with the category "-1", but additionally you can use any code number of your data matrix as mask.

Maximum scales *r* and ring width *dr*



The analysis is performed for spatial scale $r = 1, \ldots r_{max}$. The default value of the maximal scale r_{max} is half of the dimension of the smaller side of the grid; however, r_{max} can be changed with the button **set maximal radius rmax**.

If you select the *O*-ring statistic, you can change the ring width *dr* in the box **ring width**. The default ring width *dr* is one cell; however, if the rings are too narrow *Programita* will produce jagged plots for $O(r)$ as not enough points will fall into the different distance classes. In this case, you may select a larger ring width.

Background of second-order statistics

Second order statistics

Definition of the bivariate *K*- and *L*-functions

For stationary and isotropic point processes all second order characteristics can be expressed by means of the intensity λ and $K(r)$, Ripley's K function. The quantity $\lambda K(r)$ has the intuitive interpretation of the expected number of further points within distance r of an arbitrary point of the process which is not counted (Ripley 1981):

$$\lambda\, K(r) = \mathbf{E}[\#(\text{points} \le r \text{ from an arbitrary point of the pattern})] \qquad \text{(A1)}$$

where # means "the number of", and **E**[] is the expectation operator. The K-function yields under compete spatial randomness (CSR) $K(r) = \pi r^2$, which is the area of a circle with radius r. To remove the scale dependence of $K(r)$ under CSR and to stabilize the variance, a square root transformation of $K(r)$, called L-function is used instead:

$$L\,(r) = \left(\sqrt{\frac{K(r)}{\pi}} - r\right) \qquad \text{(A2)}$$

The commonly used estimator for $K(r)$ was proposed by Ripley (1976) and Ripley (1981). It is based on all distances d_{ij} between the ith and jth point of the pattern and is given by:

$$\hat{K}\,(r) = \frac{A}{n^2}\sum_{i=1}^{n}\sum_{j=1}^{n}\frac{I_r(d_{ij})}{w_{ij}} \qquad \text{(A3)}$$

where n is the number of points of the pattern in a study region of area A, I_r is a counter variable [$I_r(d_{ij})$ =1 if $d_{ij} \le r$, and $I_r(d_{ij}) = 0$ otherwise], and w_{ij} is a weighting factor to account for edge effects. The weight w_{ij} is the proportion of the area of a circle centred at the ith point with radius d_{ij} that lies within the study region (for reviews on edge correction see e.g., Haase 1995, or Goreaud & Pélissier 1999). This edge correction is based on the assumption that the region surrounding the study region has a point density and distribution pattern similar to the nearby areas within the boundary.

The bivariate quantity $\lambda_2 K_{12}(r)$ follows in a straight-forward manner and has the

intuitive interpretation of the expected number of type 2 points within distance r of an arbitrary type 1 point.

Definition of the *g*-function and of the *O*-ring statistic

The pair-correlation function $g(r)$ (Stoyan & Stoyan 1994) is related to the K-function by

$$g(r) = \frac{1}{2\pi r}\frac{dK(r)}{dr}. \qquad \text{(A4)}$$

Stoyan and Penttinen (2000) provide a heuristic definition: $g(r)$ is related to the probability $p(r)$ that each of two infinitesimally small discs dx and dy (which are a distance r away) contain a point of the process:

$$p(r) = \lambda^2 g(r)\mathrm{d}x\mathrm{d}y \qquad \text{(A5)}$$

Rearrangement of equation A4 and $\mathrm{d}K(r) = K(r+\mathrm{d}r) - K(r)$ yields

$$\lambda g(r) = \lambda\,[K(r+\mathrm{d}r) - K(r)]\,/(2\pi r\,\mathrm{d}r) \qquad \text{(A6)}$$

where $2\pi r\,\mathrm{d}r$ is the area of a ring with radius r and infinitesimal width dr. Thus, for isotropic patterns the quantity $\lambda K(r) - \lambda K(r+\mathrm{d}r) = 2\pi \mathrm{d}r\,\lambda g(r)$ may be interpreted, in analogy to equation A1, as the expected number of points in a ring with radius r and width dr centred at an arbitrary point of the process:

$\lambda\, g(r)\, 2\pi r\mathrm{d}r = \mathbf{E}$[#($r <$ points $< r + \mathrm{d}r$ from an arbitrary point of the pattern)] (A7)

where # means "the number of", and **E**[] is the expectation operator. The *O*-ring statistic

$$O(r) = \lambda g(r) \qquad \text{(A8)}$$

is thus the conditional intensity of points at distance r from an arbitrary point of the pattern.

For a homogeneous Poisson process (= CSR) $g(r) = 1$. Values $g(r) > 1$ indicate that interpoint distances around r are relatively more frequent than they would be under CSR. If this is the case for small values of r, typically there is clustering. Conversely, values $g(r) < 1$ indicate that interpoint distances around r are relatively less frequent than they would be under CSR. If this is the case for small values of r, the pattern shows regularity.

Grid-based estimators of second-order statistics

The study area is divided into a grid of cells. The size of the cells should be defined as the minimal resolution necessary to respond to the scientific question to be answered and is limited by the measurement uncertainty of point coordinates (Wiegand & Moloney 2004). The calculation of point-to-point distances necessary for estimation of second-order statistics is then based on distances between cells, and counting cells and points in cells.

Grid-based estimator of *K*- and *L*-function

Wiegand & Moloney (2004) proposed a simple grid-based estimator of the bivariate *K*-function for arbitrarily shaped study regions, which is based on the mean number of type 2 points found in (complete or incomplete) circles of radius *r* around all type 1 points *k* [= $P_{12}(r)$], divided by the area of these circles [= A(*r*)]:

$$\lambda_2 \hat{K}_{12}(r) = \pi r^2 \frac{P_{12}(r)}{A(r)} = \pi r^2 \frac{\frac{1}{n_1}\sum_{k=1}^{n_1} \mathbf{Points}_2[C_{1,k}(r)]}{\frac{1}{n_1}\sum_{k=1}^{n_1} \mathbf{Area}[C_{1,k}(r)]} \qquad \text{(A9)}$$

where $\lambda_2 = n_2/A$ is the intensity of pattern 2, n_i is the number of type i points (i = 1, 2) in the study region, $C_{1,k}(r)$ is the circle with radius *r* centred on the *k*th type 1 point, the operator. $\mathbf{Points}_2$[X] counts the points of the pattern 2 in a region X of area A, and the operator **Area**[X] determines the total number of cells of the region X.

The circles are incomplete if the focal point has a distance smaller than *r* to the border of the study region. Note that this estimator does not scale the number of points in incomplete circles to the expected number within complete circles as is commonly done in point pattern analysis (for reviews on edge correction see e.g., Haase 1995, or Goreaud & Pélissier 1999). The grid-based estimator is therefore not affected by the problem that the weights may become unbounded if *r* becomes larger.

The grid-based estimator of the *L*-function using equations A2 and A9 yields:

$$\hat{L}_{12}(r) = r\left(\sqrt{\frac{\lambda_2 \hat{K}_{12}}{\pi r^2}} - 1\right) = r\left(\sqrt{\frac{A}{n_2}\frac{P_{12}(r)}{A_1(r)}} - 1\right). \qquad \text{(A10)}$$

Grid-based estimator of *g*- and *O*-function

An analogous grid-based estimator of the bivariate pair-correlation function $g_{12}(r)$ is given by

$$\lambda_2 \hat{g}_{12}(r) = \frac{\frac{1}{n_1}\sum_{k=1}^{n_1} \mathbf{Points}_2[R^w_{1,k}(r)]}{\frac{1}{n_1}\sum_{k=1}^{n_1} \mathbf{Area}[R^w_{1,k}(r)]} \qquad \text{(A11)}$$

where $R^w_{1,k}(r)$ is the ring with radius r and width w centred on the kth type 1 point (Wiegand & Moloney 2004). For the univariate case, this estimator was e.g., used in Condit *et al.* (2000).

Selection of ring width

The estimator equation (A11) involves a technical decision on the width w of the rings. The use of rings that are too narrow will produce jagged plots, as not enough points will fall into the different distance classes. On the other hand, if the rings are too wide, the pair-correlation function will lose the advantage that it can isolate specific distance classes. More sophisticated estimators of the pair-correlation function use kernel functions such as the Epanečnikow kernel with a bandwidth h instead of rings with width w (see Stoyan & Stoyan (1994) and references therein).

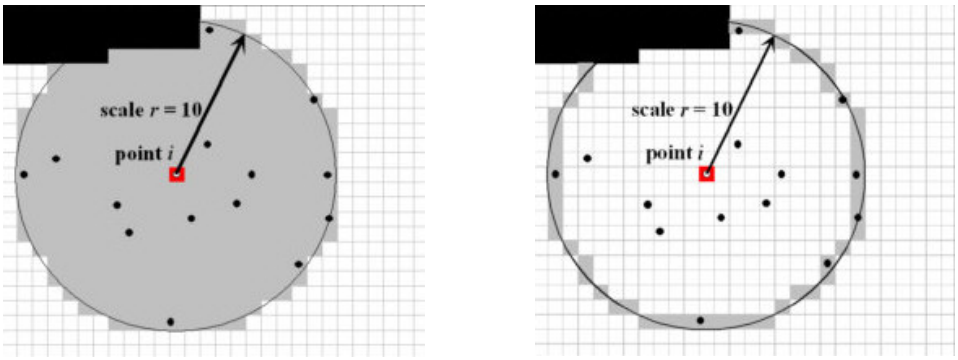


Figure A2. Numerical implementation of the *L*- function and the *O*-ring statistic for an irregularly shaped study region. Points of pattern 2 are represented by closed circles, the focal point *i* of pattern 1 as open circle within the red cell. Note that we approximate circles and rings with the underlying grid structure. Study region: grey and white cells, area outside the study region: black cells. (Left): For numerical implementation of Ripley's bivariate *L*-function we count the number of points of pattern 2 inside the part of the circles around point *i* of pattern 1 which falls inside the study region (i.e., the gray shaded area), and the number of cells within this area. (Right): For implementation of the bivariate *O*-function we count the number of points of pattern 2 inside the part of the ring around point *i* of pattern 1 which falls inside the study region (i.e., the gray shaded area), and the number of cells within this area.

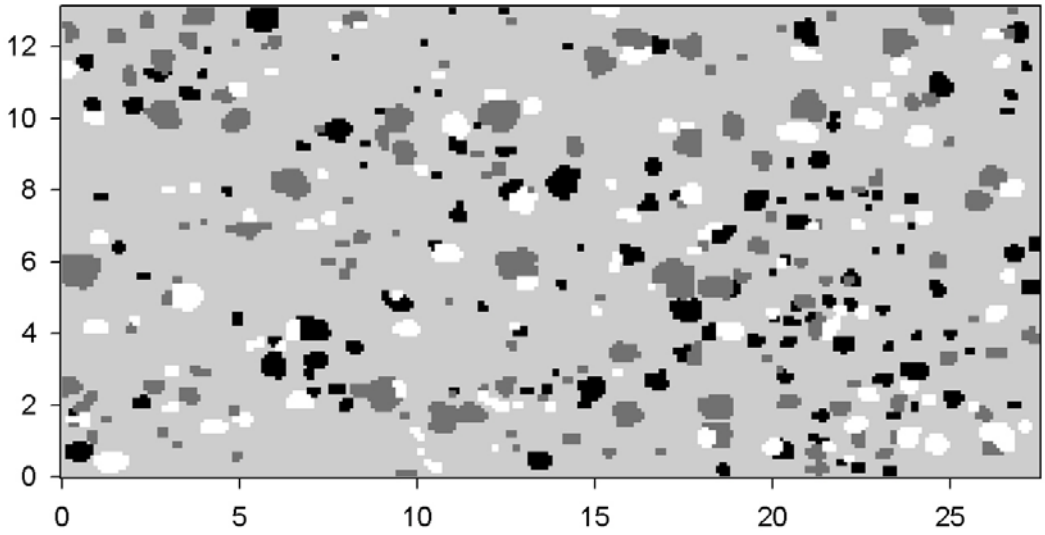


Figure F1. Categorical map of a 27.4m × 13m study plot in the semiarid grass-shrub steppe in Patagonia (Argentinia), showing individuals of the dominant shrub species *Adesmia campestris* (black), *Mulinum spinosum* (dark grey), and *Senecio filaginoides* (white). Each cell is 10cm × 10cm.

Considering finite size and irregular shape

One of the limitations of point pattern analysis in plant ecology is that the plants are idealized as points. The point approximation is valid where the size of the plants is small in comparison with the spatial scales investigated, but may obscure the real spatial relationships at smaller scales, the relationship in which ecologists are mostly interested when interactions among plants are studied.

Programita contains an extension of the grid-based approach to point-pattern analysis (Wiegand & Moloney 2004) to deal with objects of finite size and irregular shape. The basic idea is to represent plants in a study area by means of a categorical raster map with a cell size smaller than the size of the plants. A plant is represented by one or several adjacent grid cells, depending on its size and shape, in a map representing categories such as bare ground, cover of species 1, cover of species 2 and so on (figure F1).

The simple grid-based estimators of the bivariate functions K_{12}, L_{12} and $g_{12}(r)$ (eqn A9, A10, and A11) can be easily extended to allow analysis of categorical raster maps such as Figure F1. The size of the smallest plants, or other criteria for a minimal required resolution, is used to define an appropriate size for the cells. To calculate the second-order statistics of categorical maps with the estimators given in equations A10, and A11, a point pattern is formally constructed from the map (Fig. F2):

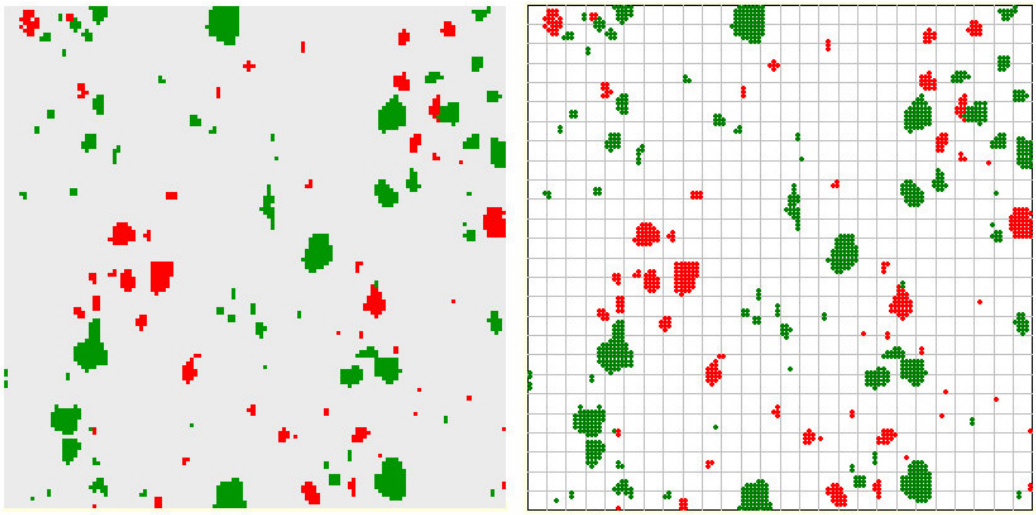


Figure F2. Left: categorical map with a bivariate pattern (red: shrubs of species 1, green: shrubs of species 2). Right: Point pattern formally constructed from the categorical map shown on the left. Note that the grid lines indicate 5 × 5 blocks of cells and not the cell size.

A given cell obtains one type 1 point if it is covered by one of the categories assigned to pattern 1 (e.g. all shrub species) and one type 2 point if it is covered by one of the categories assigned to pattern 2 (e.g. all grass species), but is classed as empty if it is not covered by either pattern 1 or 2 but is located within the study area, and is assigned to the "mask" if the cell is outside the study area.

Although this approach corresponds with conventional point pattern analysis, the explicit consideration of real world structures (i.e. objects of finite size and irregular shape) prevents an analytical treatment. This extension is therefore a simulation-based approach for testing specific "ad hoc" hypotheses about the spatial dependencies of objects in a particular system.

Randomization of objects finite size and real shape

The key for successful application of *Programita* is the selection of an appropriate null model that responds to the specific biological question asked. The approach for dealing with objects of finite size and irregular shape allows for testing specific null models adapted to the biology of the study system and provides a considerable degree of added realism. However, remember that the null model constitutes a point of reference against which the data are compared. Therefore the null model must not necessarily describe all particularities of the real system.

Specific null hypotheses on the considered system can be tested through analysis of the spatial pattern of plants with real shape and finite size. For example, are plants of a given species randomly (but without overlaps) distributed over the study area, are the spatial patterns of two species independent, or do plants of species 2 suffer competition (or facilitation) from plants of species 1? In a later section we present several important benchmark null models to address these questions.

Although conceptually analogous to the most simple null models in point pattern analysis (i.e., CSR, heterogeneous Poisson, independence, random labelling, and antecedent condition; Wiegand & Moloney 2004), consideration of the finite size and irregular shape of plants requires specification of more biological detail. Specifically, we need to introduce rules and options to decide on the overlap between plants, explain how to construct objects from a categorical map, how to randomize the position of the objects, and how to take edge effects into account which may arise if randomized objects partly overlap the limits of the study region. How this is implemented in *Programita* is explained in the following.

Overlap between plants

An important difference between conventional point-pattern analysis and analysis of categorical maps is that points cannot overlap (except where they occupy exactly the same location), but for randomisation of the position of plants of finite size rules are needed to determine if they are allowed to overlap or not.

Since a category (and not a number of points) is assigned to each cell, overlap of two plants of the same pattern is not allowed. (However, to avoid that several small plants may occupy the same grid cell the size of the grid cell may be reduced.)

Depending on the null hypothesis, we may (or may not) allow overlap of plants of two different patterns. This difference is important for data collection and mapping, as for the application of null models. For example, allowing overlap of the two component patterns of a bivariate pattern is relevant for a null model to approximate, for instance, "third dimension" effects which may occur if smaller plants such as grass tufts grow inside larger unpalatable shrubs.

After selecting "Matrix" in How are your data organized?, "Data are given as matrix map" in Select modus of data, and after specifying in the window Give code numbers

for pattern which code numbers of your data matrix make up pattern 1, pattern 2, and the mask, apply the check box "Calculate confidence limits". A window for selection of the null model appears (Figure N1) appears. The check box "Only one point per cell" is always enabled in the matrix mode. To allow overlap of objects of pattern 1 and pattern 2 enable the check box "Only one point per pattern".

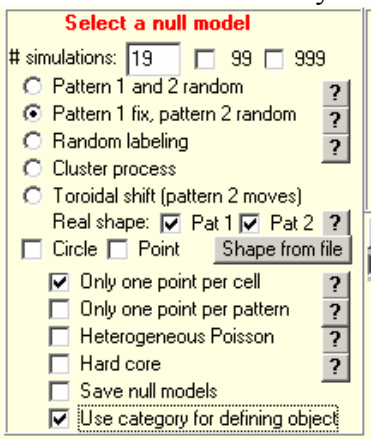


Figure N1. Window for selection of null model

Figure N2 top right shows a randomization of pattern 2 without overlap to pattern 1 (null model "Pattern 1 fix, pattern 2 random"), and figure N2 bottom shows randomization of pattern 2 with the same null model but allowing overlap to pattern 1.

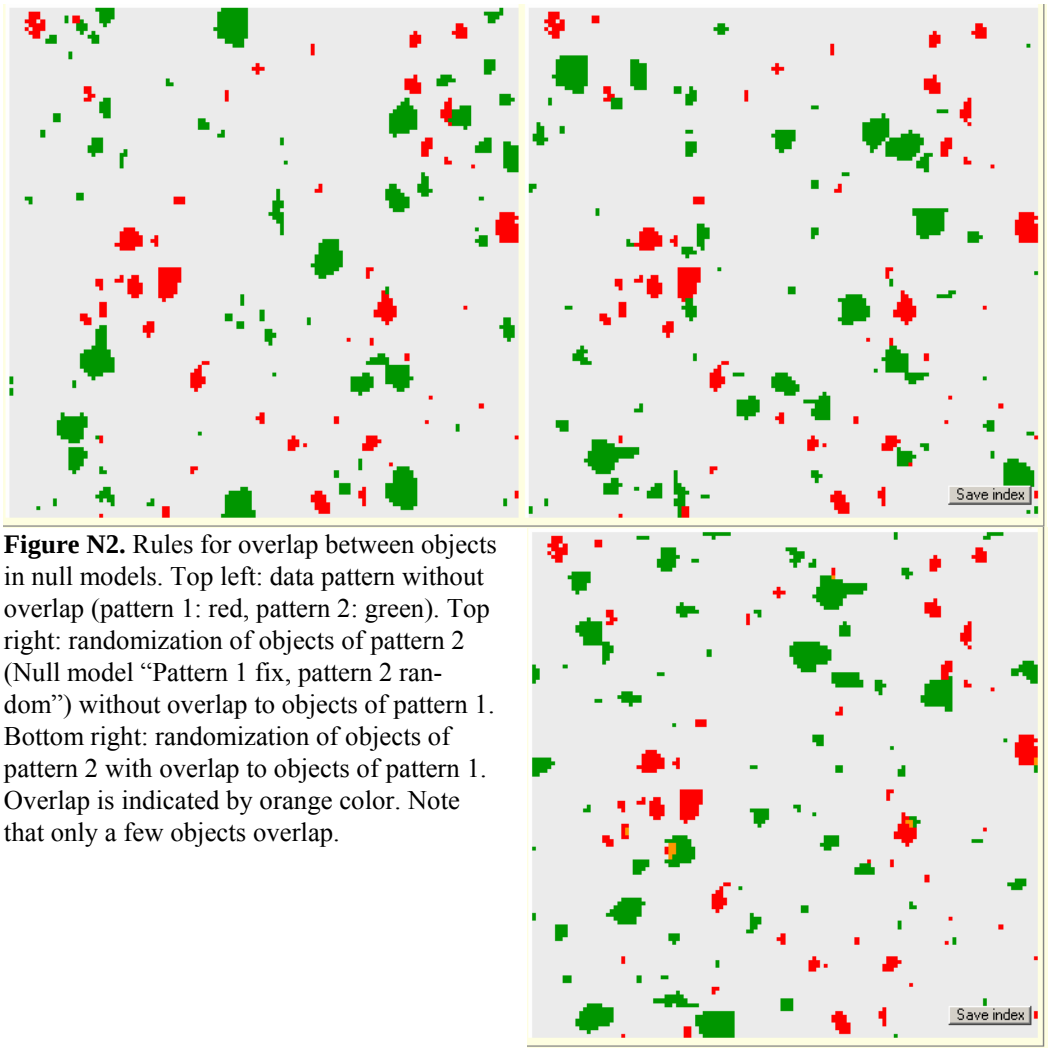


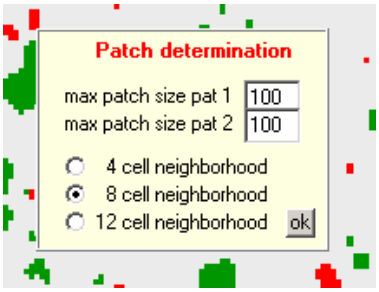
Figure N2. Rules for overlap between objects in null models. Top left: data pattern without overlap (pattern 1: red, pattern 2: green). Top right: randomization of objects of pattern 2 (Null model "Pattern 1 fix, pattern 2 random") without overlap to objects of pattern 1. Bottom right: randomization of objects of pattern 2 with overlap to objects of pattern 1. Overlap is indicated by orange color. Note that only a few objects overlap.

Construction of objects from categorical map

A categorical map, such as figure N2 top left, contains intuitively discernable discrete objects; however, in order to randomize the position of these objects for a given null model *Programita* must first define objects. This is done with a percolation algorithm which summarizes all adjacent cells of the same type (i.e., type 1 or type 2) as one object.

If pattern 1 of your categorical map comprises objects of finite size and irregular shape, enable in the window for the selection of the null model (figure N1) the check box "Pat1". If pattern 2 of your categorical map comprises objects of finite size and irregular shape, enable additionally check box "Pat2". After enabling "Pat1" and/or "Pat2", a small window "Patch determination" opens which allows you to select specific settings for the definition of the objects.

First, to avoid very large objects, you can define a maximal size of the objects, given in number of cells (max patch size pat 1, and max patch size pat 2). If you e.g., select 100, the algorithm assigns the first encountered 100 adjacent cells to a given object, but does consider further adjacent cells as a separate object.



Second, there are three different neighbourhoods used to define adjacency to a given cell:

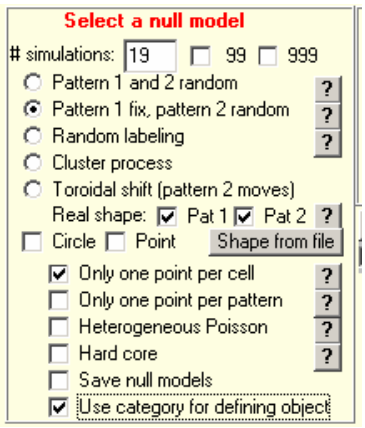
- the 4 cell neighbourhood includes only the four immediate (north, east, south, west) neighbours,
- the 8 cell neighbourhood includes the eight immediate neighbours including the four diagonal neighbours,
- the 12 cell neighbourhood includes the eight immediate neighbours and additionally the four next (north, east, south, west) neighbours.

The 4 and 8 cell neighbourhood assigns only cells which touch directly to objects, whereas the 12 cell neighbourhood allows you to have objects with small gaps.

Separation of joined objects

In some cases discrete objects of a given pattern may touch each other. In this case the automatic algorithm implemented in *Programita* will join the two objects to one single object.

One possibility to avoid this problem is to create a new category for touching objects and to enable the check box "Use category for defining objects".



In this case *Programita* will base the definition of the objects not only on cells occupied by pattern 1 (or pattern 2), but additionally on the category of the cells in your original map. In this case an object can only comprise cells of the same category.

Another simple possibility to avoid the problem of joined objects is dividing the cells into 4 smaller cells and leaving empty cells between adjacent but distinct objects. Finally, you may manually separate objects.

Manual separation of joined objects

To manually separate objects run first one analysis where adjacent but separate objects may be joined by *Programita*. Use the temporal files temppatch1.dat and temppatch2.dat which are automatically created by *Programita* and change the name of temppatch1.dat to name.pa1 and temppatch2.dat to name.pa2 (for name use an appropriate name). The subfix *.pa1 and *.pa2 are reserved for manually modified files containing the information on the objects of pattern 1 and pattern 2, respectively.

These files are the "object" representation of your data of pattern 1 and pattern 2. The first line in the files gives the number of objects of pattern 1 (or pattern 2), the next lines contain the information on the objects (each object is a line) necessary for randomization of the objects of finite size and irregular shape.

The first two columns are the minimal x- and y- coordinates of the object, the third column gives the width of the object in x-direction (= xmax - xmin), the fourth column gives the width of the object in y-direction (= ymax - ymin), the

fifth column the number of cells of the objects, and the following columns give the pairs of coordinates belonging to the object.

For example, the beginning of the temppatch1.dat may be given by:

```
1
   1   185   2   2   6   1  186   1  187   2  186   2  187   2  185   3  186
```

This indicates that there is **1** object, and the minimal x- and y-coordinates of the object are **1** and **185**, respectively. The width in x- and y-direction of the object is **2** cells (xmax= 3, xmin=1; ymax=187, ymin = 185), and the object comprises **six** cells (1, 186), (1, 187), (2, 186), (2, 187), (2, 185), and (3, 186). This is the objects with its coordinates:

```
   185  186  187
1|      X    X
2|  X   X    X
3|      X
```

You can now split this object manually into two objects:

object 1 with coordinates: (1, 186), (1, 187), (2, 187), and
object 2 with coordinates: (2, 186), (2, 185), (3, 186):

```
   185  186  187          185  186  187
1|      X    X       1|
2|           X       2|  X   X
3|                   3|      X
```

To split them you need to modify the file accordingly:

```
2
   1   186   1   1   3   1  186   1  187   2  187
   2   185   1   1   3   2  186   2  185   3  186
```

i.e., adding one objects (**2**), changing the **minimal x- and y-coordinates**, the **width**, the **number of cells belonging to the object**, and the coordinates of the cells.

To help you with this task, *Programita* creates two temporal files temppatchNr1.dat and temppatchNr2.dat which are a matrix representation of pattern 1 and pattern 2, respectively, but every object is coded with a number numbered according to the order in the list of objects given in temppatch1.dat and temppatch2.dat:

The beginning of temppatch1.dat is:

```
49
 5 2 4 6 23  5 4  6 4  6 5  6 3 7 4 7 5 7 3 7 6 5 6 6 2 7 2 8 5 8 3 8 6 8 2 7 7 8 7 6 7 9 5 9 6 9 4 7 8 8 8
17 3 1 1  4 17 3 17 4 18 3 18 4
```

The corresponding part of temppatchNr1.dat is:

```
1   130  1   130
    0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0   y =1
    0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0   y =2
    0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0   y =3
    0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0   y =4
    0 0 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0   y =5
    0 1 1 1 1 0 1 0 0 0 0 0 0 0 0 0 0 0   y =6
    0 1 1 1 1 1 1 1 0 0 0 0 0 0 0 0 0 0   y =7
    0 1 1 0 1 1 1 1 0 0 0 0 0 0 0 0 0 0   y =8
    0 0 0 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0   y =9
    0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
    0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
    0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
    0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
    0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
    0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
    0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
    0 0 2 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0
    0 0 2 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0
    0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

x:  1 2 3 4 5 6 7 8 9 ......
```

Note that the matrix counts the x-axis from left to right, and the y-axis from top to bottom. Therefore, the minimal coordinates of object 1 are (5, 2), and of object 2: (17, 3).

Randomization of the position of objects

Several null models require randomisation of the position of the objects. In conventional point-pattern analysis this is easy: randomisation of points involves only assignation of random coordinates. However, a plant of finite size may occupy several adjacent cells and its shape needs to be preserved.

Programita achieves this by rotating the objects by 0, 90, 180, or 270 degrees (each of the four variants being equally probably) and by randomly shifting the rotated plant as a whole (Figure N3).

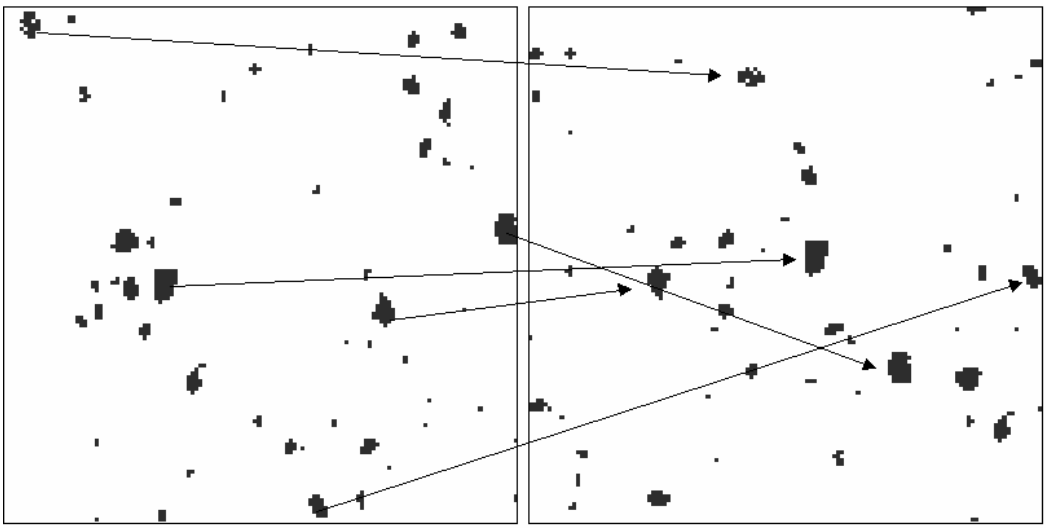


Figure N3. Randomization of position of objects. Left: data pattern, right: randomization of position of original objects of the data pattern. Arrows indicate for some objects their rotated and moved counterparts of the null model.

Edge correction if objects fall partly outside the study rectangle

The finite size of the plants requires edge correction since randomly displaced plants may fall partly outside the arbitrarily selected study rectangle. This would reduce in the null model the proportion λ of occupied cells and produces a (positive) bias towards aggregation. Programita includes three methods to mitigate this effect (figure N4).

Plants are not allowed to fall outside.— Randomized plants are not allowed to fall partly outside the study rectangle. This produces a negative bias towards regularity since fewer plants of the null model are distributed close to the border. Thus, the intensity of cells simulated by the null model is smaller at the border and larger in the inner parts of the plot (Figure N5).

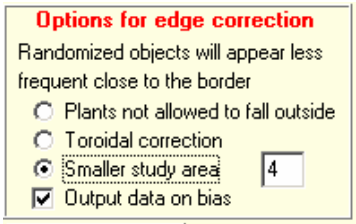

Options for edge correction
Randomized objects will appear less frequent close to the border
Plants not allowed to fall outside
Toroidal correction
Smaller study area
4
Output data on bias

Figure N4. Option window for edge correction applied for randomization of position of objects

Toroidal correction.— The second method avoids the negative bias produced by the first method by treating the rectangular study plot encompassing the study region as a torus, i.e., the part of a plant outside the rectangle is made to appear at the corresponding opposite border. However, breaking relatively large plants into two smaller plants produces a slight positive bias.

Smaller study area.— A third method uses the torus correction, but calculates the second-order statistics only inside an inner rectangle excluding cells close to the border (guard area). You can select the wide of the guard area (figure N4).

For a guard area wider than the diameter of the largest plants the biases of the first and the second method disappear, but this may reduce the size of the study rectangle considerably. Therefore, the guard area may be selected wider than the diameter of most plants, but still small enough to yield a large enough study rectangle.

To randomise the plants of a given pattern under the above rules, *Programita* performs repeated trials for each individual plant. If the provisionally distributed plant (which was randomly mirrored and shifted) overlaps with an already distributed plant of the same pattern (or the other pattern if appropriate) or falls partly outside an irregularly shaped study area this trial is rejected. The procedure is repeated until a location is found where both rules are met.

Test of possible bias through edge correction

Programita allows you to assess the magnitude of possible bias in the distribution of objects relative to the border of the study area. If you enable the check box "Output data on bias" in the Option window for edge correction (FigureN4), the results file will contain at the end the line "DistDistanceToBorder" which gives the total number of cells with x-coordinate x that were occupied by an object randomized during any simulation of the null model:

```
DistDistanceToBorder 0,1,2...  0  63 139 203 268 301 310 322 330 369 403 416 ...
```

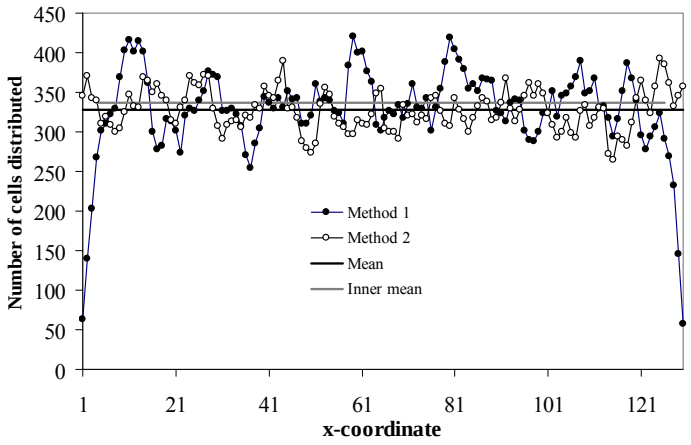


Figure N5. Distribution of objects of finite size relative to the borders of the study area. Shown is the total number of cells in 99 simulations (of the null model shown in figure N3) which were occupied by a cell of pattern 1. Filled circles: method "Plants are not allowed to fall outside", open circles: method "Toroidal correction". Horizontal: expected number of cells.

Figure N5 shows that with method 1 "Plants are not allowed to fall outside" there are less objects of pattern 1 close to the border (filled circles, x-coordinates 1, 2, 3, and 4, and 127, 128, 129, and 130) as expected (horizontal line) because objects partly overlapping the border of the study area are rejected. However, more than 4 cells away from the border the objects are randomly distributed. Consequently, the inner mean (gray horizontal) is slightly elevated. This is because hardly an object has a diameter larger than 4 cells (figure N3). The bias for cells closer than 4 cells from the border disappears for the method 2 "Toroidal correction" (open circles in figure N5). Note that the size of the objects and the condition that they are not allowed to overlap leads to fluctuations in the density.

The third method of edge correction uses the second method (Toroidal correction), but measures the second-order properties only inside an inner rectangle excluding cells close to the border (guard area). Because the objects are randomly distributed, this leads to a slightly fluctuating number of cells belonging to pattern 1 of the null model inside the inner rectangle. To check the degree of fluctuation (which may become large if the inner rectangle is small) the results file contains at the end a line "Anzpat1" and "Anzpat2" which gives the number

of cells of pattern 1 and pattern 2, respectively, in each replicate simulation of the null model:

```
Anzpat1= 364 350 427 406 407 342 371 349 362 375 383 373 374 376 397 378
```

Masking (space limitation)

Competition for space is an important ingredient of null models for plants with finite size. We may encounter situations where plants of the focal species cannot inhabit some areas of the ground, e.g., if it is already occupied by other species. Programita allows considering restrictions in the accessible space in an easy way. All non-accessible cells are summarized as a third pattern (called "mask") and are excluded from the study region. The mask may be cells already indicated by code -1 (*.dat) or code -9999 (*.asc) as cells outside the study area, but can be any other code number, e.g., a third species. The mask can be enabled by selecting "Irregularly shaped study region" in the settings menu Give modus of analysis.

Note that in the case of an irregularly shaped study region the edge correction method 1 (Plants are not allowed to fall outside) is automatically enabled; the two other two options do not make sense.

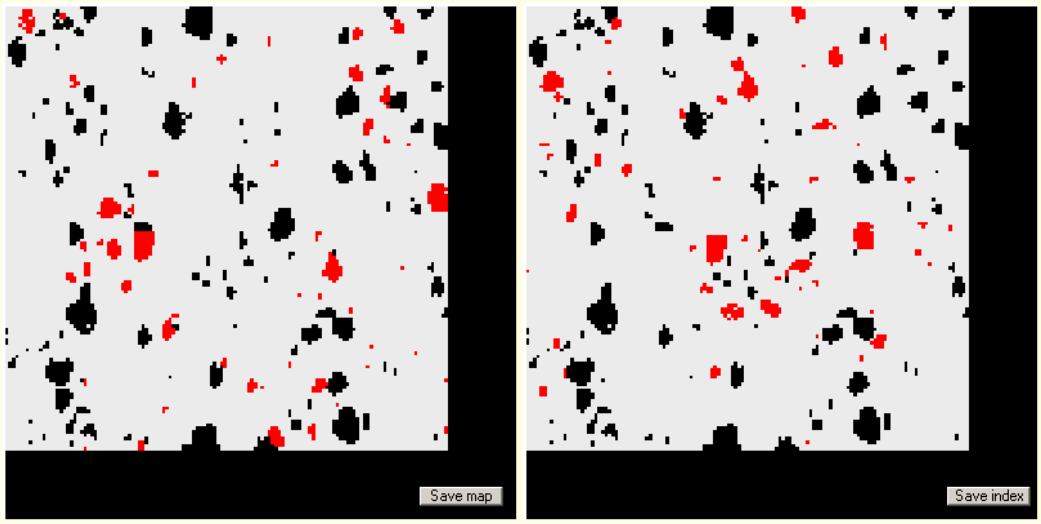
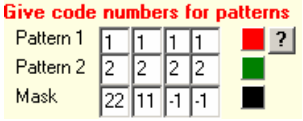


Figure N6 Masking. Data file m_ter_22.dat. Two strips in the left and in the bottom of the plot are excluded (code 11) and shrubs of other species as well (code 22).



Circle approximation

Programita offers an option to analyze the effect of the irregular shape by approximating objects with irregular shape by circular objects of the same size. To this end enable the check box “Circle” in the window for specifying the null model below the real shape check boxes.

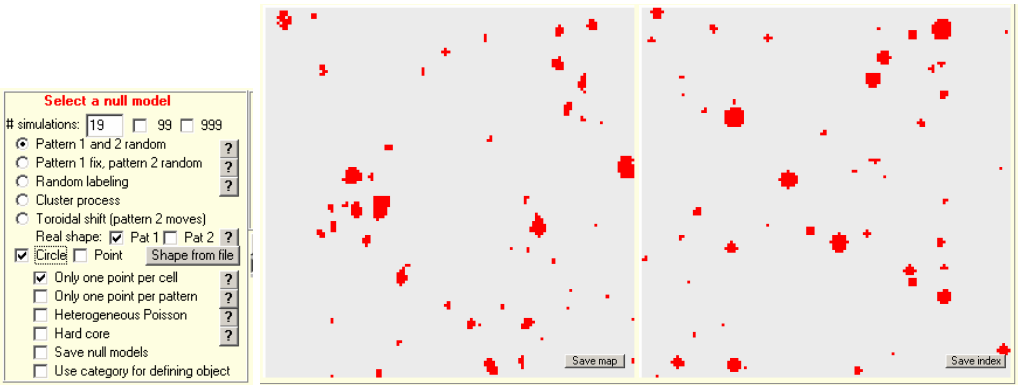


Figure N7. Circle approximation. Left: data with objects of irregular shape, right: null model with approximation of objects by circle of same size. Note that the circles are sometimes not perfectly circular because they have to be approximated by the underlying grid.

Point approximation

Programita offers an option to compare the analysis with objects of finite size and irregular shape to the common point approximation. *Programita* approximates the objects by a point with coordinates being the average x- and y- coordinates of the cells belonging to the object.

To this end enable the check box “Point” in the window for specifying the null model below the real shape check boxes.

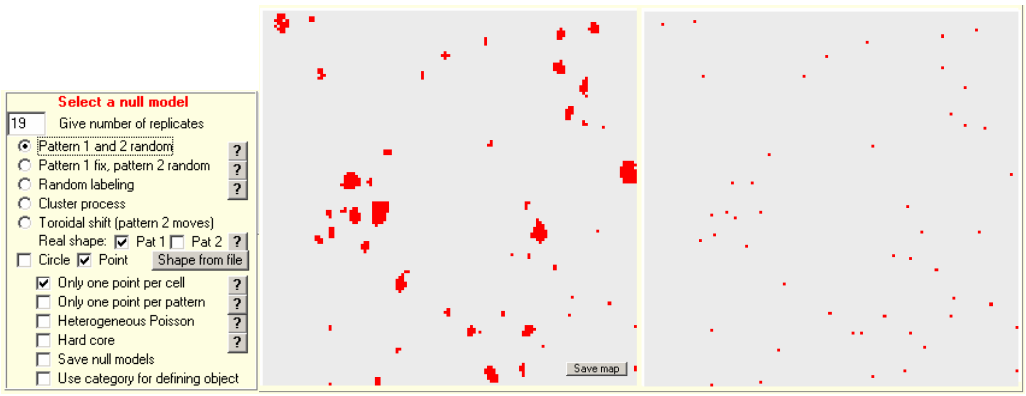


Figure N7. Point approximation. Left: data with objects of irregular shape, right: Point approximation of data shown on the left.

Null models for objects with finite size and irregular shape

Although the null model for finite size and irregular shape are conceptually analogous to the most simple null models in point pattern analysis (i.e., CSR, heterogeneous Poisson, independence, random labelling, and antecedent condition; Wiegand & Moloney 2004), consideration of the finite size and irregular shape of plants requires specification of more biological detail. In the last section we provided all technical details for definition of the null models, in the following we will present several examples for null models which use the feature of categorical maps and objects of finite size and irregular shape.

CSR: Randomising plant position for univariate patterns

The most simple and most widely used null model for univariate point patterns is complete spatial randomness (CSR) where any point of the pattern has an equal probability of occurring at any position in the study area, and the position of a point is independent of the position of any other point (i.e., there is no interaction). Plants of finite size and irregular shape are, in analogue to CSR, distributed randomly as described above. This null model operates as a dividing hypothesis to detect further regularity or aggregation in univariate patterns.

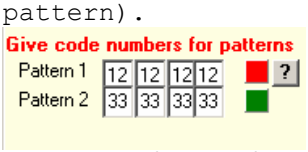
CSR and rectangular study region (Example F_CSR_1.res)

CSR is the basic null model for univariate patterns and most settings for CSR will apply equally for other univariate null models. Therefore, we explain all steps of the analysis for CSR in detail, but skip some of these details in the description of the other univariate null models.

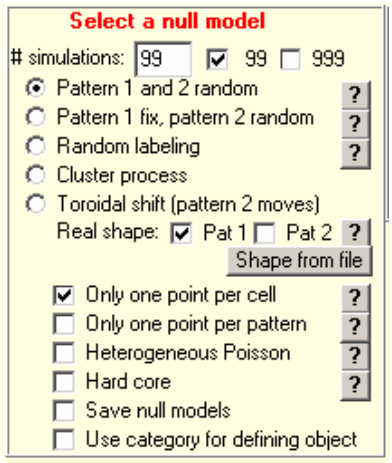
Input data file: Figure2.asc
How are your data organized: Matrix
Give modus of analysis Analyze all data in rectangle
Which method will you use? Ring (or Circle)
Ring width: 1 (if intensity λ of cells is too low, select larger ring widths)
Set maximal radius rmax: 30 (too large scales slow down *Programita*)
Select modus of data: Data are given as matrix map
Give code numbers for pattern: Pattern 1:12 12 12 12 (shrub species *Mulinum spinosum*)
Pattern 2: 33 33 33 33 (code does not occur)

---

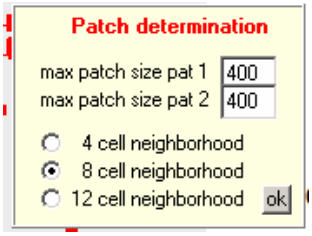
1) highlight the data file "Figure2.asc" in the window **Input data file**
2) select "Matrix" in **How are your data organized**
3) select "Analyze all data in rectangle" **in Give modus of analysis**
4) select the code numbers for pattern 1 and pattern 2 in **Give code numbers for patterns**: write 12 in all windows reserved for pattern 1 (the species *Mulinum spinosum*) and write 33 in all windows reserved for pattern 2 (the code 33 does not occur in Figure2.asc, therefore you define a univariate pattern).

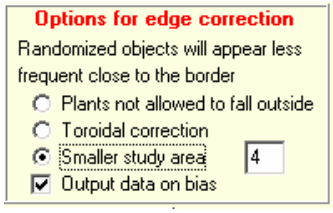


5) select "Ring (Wiegand-Moloney)" in **Which method will you use?** if you like to use the *O*-ring statistic [and Circle (Ripley) if you like to use the *L*-function]
6) select an appropriate ring width *dr* in the box **ring width**. Usually a ring width of one cell is appropriate, however, if the intensity λ of points in the study region is too low, the graph of the *O*-ring statistic will be jagged and selection of a larger ring width *dr* is appropriate
7) click the button "change" in **set maximal radius rmax** to define the maximal scale *r* of the analysis and insert "30". A too large scale r_{max} will slow down *Programita*.
8) select "Data are given as matrix map" in **Select modus of data**
9) Click button "Calculate index". Your pattern appears on the left, and the *O*-ring function of your data appears on the right.
10) To determine Monte Carlo confidence limits for CSR, enable the check box "Calculate confidence limit" on the upper left. A window with settings for null models appears. Select "Pattern 1 and 2 random":

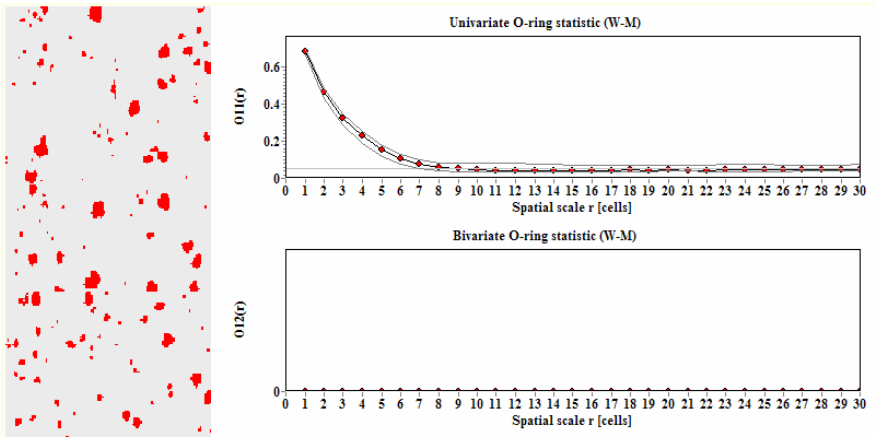


11) You can change the number of replicate simulations of the null model in the box "# simulations". If you want to use the 5th lowest and highest values of 99 (or 999) Monte Carlos simulations as confidence limits enable the check box "99" or "999".
12) Enable check box "Pat1" to activate the real shape modus where *Programita* recognizes objects of several adjacent cells. Two windows open, **"Patch determination"** appear on the left over the map and **"Options for edge correction"** right of the window for specification of the null model:




Options for edge correction
Randomized objects will appear less frequent close to the border
Plants not allowed to fall outside
Toroidal correction
Smaller study area
4
Output data on bias

13) Select in window "Patch determination" the maximal size of a shrub of pattern 1 (select 400 as very large value), and the type of neighborhood and confirm with "ok".
14) Select in the window "options for edge correction" the rules for randomization of the objects.
15) Press "Calculate index". Now *Programita* performs the simulations of the CSR null model and shows you the pattern of the Monte Carlo null models. After termination of the simulations of the null model a graph appears, showing the *O*-ring function of your data (left) and the confidence limits of your null model (right):



16) To save the results of the analysis, press the button "Save results", which appears below the graph with the results of the univariate analysis, and insert a name for the result-file. The results-file will be saved as ASCII-file with a *.res extension in the same directory where programita.exe is located. It contains the settings of your analysis and the results of the univariate (and the bivariate) point-pattern analysis.
17) *Programita* uses as default the lowest and highest $O(r)$ of the different simulations of the null model as confidence limits. However, it automatically produces two temporally files (Uni_confidence.env, Bi_confidence.env) that contain the $O(r)$ for all simulations of the null model. The columns of these files are the scales $r_0 = 1$, r_{max}, and the lines are the different simulations of the null model. The temporary files are overwritten if you start a new analysis.

CSR in irregularly shaped study region with mask (Example F_CSR_2.res)

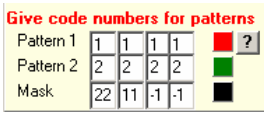
This example shows application of the mask. Competition for space is an important ingredient of null models for plants with finite size. One may encounter situations where plants of the focal species cannot inhabit some areas of the ground, e.g., if it is already occupied by other species. *Programita* facilitates an elegant extension of the null models CSR and antecedent condition to consider restrictions in the accessible space. All non-accessible cells are summarized as a third pattern (called "mask") and are excluded from the study region.

Masking is especially important for the null model antecedent condition. Not considering the plants of the third pattern will reduce the intensity of pattern 2, which then appears to be aggregated in respect to pattern 1. For univariate analysis (i.e., CSR) this effect is only important if larger continuous areas are non-accessible (e.g., example in Wiegand & Moloney 2004).

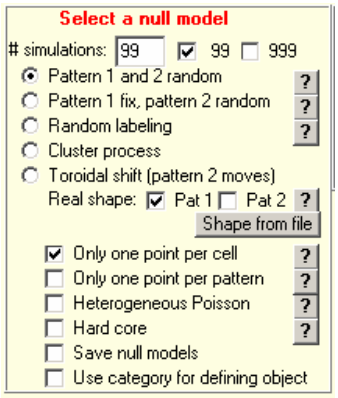
Input data file: m_ter_22.dat
How are your data organized: Matrix
Give modus of analysis Irregularly shaped study region
Which method will you use? Ring (or Circle)
Ring width: 1 (if intensity λ of cells is too low, select larger ring widths)
Set maximal radius rmax: 30 (too large scales slow down *Programita*)
Select modus of data: Data are given as matrix map
Give code numbers for pattern: Pattern 1: 1 1 1 1 (shrub species 1)
Pattern 2: 2 2 2 2 (code does not occur)
Mask: 22 11 -1 -1 (22: other shrubs, 11: outside strips)

---

1) Highlight the data file "m_ter_22.dat" in the window **Input data file**
2) select "Matrix" in **How are your data organized**
3) Enable the check box "Irregularly shaped study region".
4) Select the code numbers for pattern 1, pattern 2, and the mask in **Give code numbers for patterns**: write 1 in all boxes reserved for pattern 1 (shrub species 1) and write 2 in all boxes reserved for pattern 2 (the code 2 does not occur in m_ter_22.dat, therefore you define a univariate pattern), write in the boxes reserved for the mask 22 (other shrub species) and 11 (the outside strips):

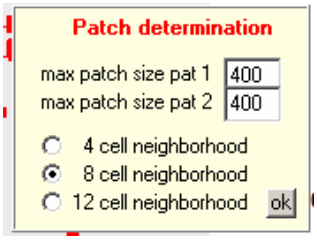


5) Click button "Calculate index". Your pattern appears on the left, and the *O*-ring function of your data appears on the right.
6) To determine Monte Carlo confidence limits for CSR, enable the check box "Calculate confidence limit" on the upper left. A window with settings for null models appears:

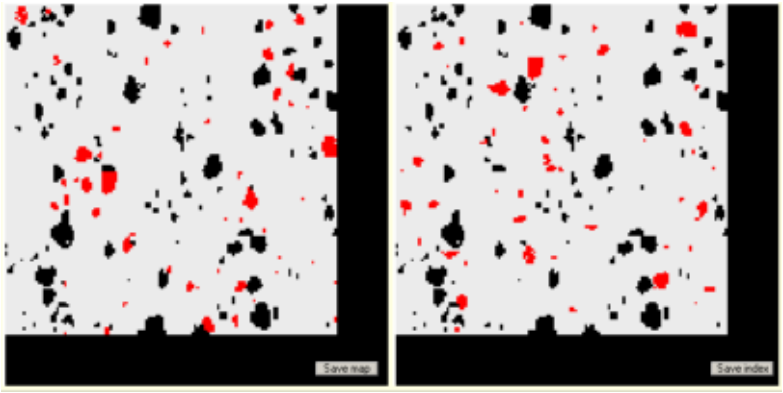


Select "Pattern 1 and 2 random".

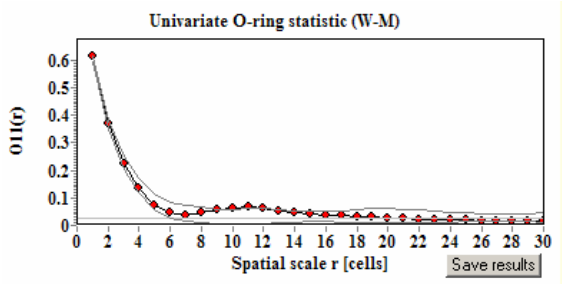
7) You can change the number of replicate simulations of the null model in the box "# simulations".
8) Enable check box "Pat1" to activate the real shape modus where *Programita* recognizes objects of several adjacent cells. A windows opens:



9) Select in window "Patch determination" the maximal size of a shrub of pattern 1 (select 400 as very large value), and the type of neighborhood and confirm with "ok".
10) Press "Calculate index". Now *Programita* performs the simulations of the CSR null model and shows you the pattern of the Monte Carlo null models. The objects do not overlap the black "holes" made by the other species and are only distributed inside the smaller study region.



11) After termination of the simulations of the null model a graph appears, showing the confidence limits of your null model (right). There is a slight clustering at scales r = 10, 11, and 12:



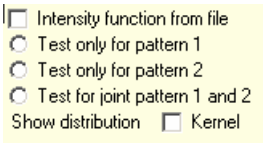
Heterogeneous Poisson null model (HP)

If a univariate point pattern is not homogeneous (i.e., the first order intensity of the pattern is not approximately constant), the null model of CSR is not suitable for exploration of second-order characteristics, and a null model accounting for first-order effects has to be used to reveal "true" second-order effects.

A common assumption is that small-scale departures from homogeneity (CSR) are due to interactions among the points whereas larger-scale departures are due to exogenous factors. Unfortunately, large-scale heterogeneity critically influences the second-order characteristics at smaller scales and appropriate null models need to be used to reveal the "true" second order characteristics; see for example the discussion on "virtual aggregation" in Wiegand and Moloney (2004).

The heterogeneous Poisson process is the most simple alternative to CSR if the point pattern shows first-order effects. The constant intensity of the homogeneous Poisson process is replaced by a function $\lambda(x, y)$ that varies with location (x, y), but the occurrence of any point remains independent of that of any other (Pélissier & Goreaud 2001; Wiegand & Moloney 2004).

The grid-based approach allows for straightforward generalization of a heterogeneous Poisson null model for objects of finite size if the heterogeneity occurs for scales well above the size of the plants. The intensity function $\lambda(x, y)$ is estimated using a kernel estimate (e.g., Bailey & Gatrell 1995; Diggle 2003; Wiegand & Moloney 2004). *Programita* includes two different kernel functions for estimating the intensity function $\hat{\lambda}^R(x, y)$: a moving window estimate (the default) and an estimate using the Epanečnikov kernel. To use the Epanečnikov kernel enable the check box "kernel":


Intensity function from file
Test only for pattern 1
Test only for pattern 2
Test for joint pattern 1 and 2
Show distribution
Kernel

The first method implemented in *Programita* uses a moving-window estimate of the non-constant first-order intensity $\lambda(x, y)$:

$$\hat{\lambda}^R(x,y) = \frac{\textbf{Points}[C_{(x,y)}(R)]}{\textbf{Area}[C_{(x,y)}(R)]} \qquad \text{(HP1)}$$

where $C_{(x, y)}(R)$ is a circular moving window with radius R that is centered in cell (x, y), the operator $\textbf{Points}_2[X]$ counts the points of pattern 2 in a region X, and the operator **Area**[X] determines the area of the region X. As edge correction, the number of points in an incomplete circle is divided by the proportion of the area of the circle that lies within the study region. This is a simple kernel estimate with the kernel function:

$$e_R(d) = \begin{cases} 1 & 0 \le d \le R \\ & \\ 0 & d > R \end{cases} \qquad \text{(HP2)}$$

where d is the distance between the focal cell and the counted cell and R the bandwidth. The second method uses an Epanečnikov kernel recommended by Stoyan and Stoyan (1994):

$$e_h(R) = \begin{cases} \frac{3}{4h}(1-\frac{d^2}{R^2}) & 0 \le d \le R \\ & \\ 0 & d > R \end{cases} \qquad \text{(HP3)}$$

All points x_i surrounding a given location x were counted within distance R, but weighted with the kernel $e_R(d)$, where d is the distance between locations x and x_i. In general, the Epanečnikov kernel produces a smoother intensity function than the mowing window estimate. An appropriate bandwidth R needs to be larger than the typical size of the plants but smaller than the range over which the environmental gradient may vary.

For implementation of the heterogeneous Poisson process a given plant is provisionally placed at a random location of the study region, but this plant is only retained with a probability proportionally to $\hat{\lambda}^R(x,y)$, averaged over all cells of the plant. This procedure is repeated until n points are distributed.

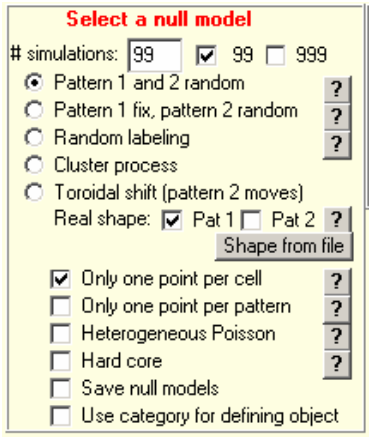
Heterogeneous Poisson (Example F_HP_1.res)

This example applies a heterogeneous Poison null model to the previous example.

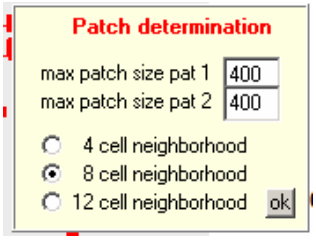
Input data file: m_ter_22.dat
How are your data organized: Matrix
Give modus of analysis Irregularly shaped study region
Which method will you use? Ring (or Circle)
Ring width: 1 (if intensity λ of cells is too low, select larger ring widths)
Set maximal radius rmax: 30 (too large scales slow down *Programita*)
Select modus of data: Data are given as matrix map
Give code numbers for pattern: Pattern 1: 1 1 1 1 (shrub species 1)
Pattern 2: 2 2 2 2 (code does not occur)
Mask: 22 11 -1 -1 (22: other shrubs, 11: outside strips)

---

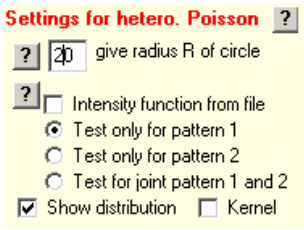
1) Click button "Calculate index". Your pattern appears on the left, and the *O*-ring function of your data appears on the right.
2) To determine Monte Carlo confidence limits for CSR, enable the check box "Calculate confidence limit" on the upper left. A window with settings for null models appears:



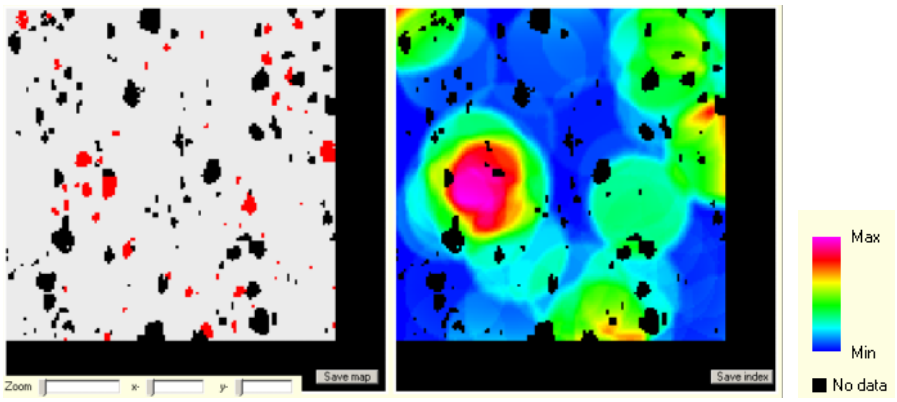
Select "Pattern 1 and 2 random".
3) You can change the number of replicate simulations of the null model in the box "# simulations".
4) Enable check box "Pat1" to activate the real shape modus where *Programita* recognizes objects of several adjacent cells. A windows opens:



5) Select in window "Patch determination" the maximal size of a shrub of pattern 1 (select 400 as very large value), and the type of neighborhood and confirm with "ok".
6) Enable the check box "Heterogeneous Poisson" in the null model window. A small settings window for the heterogeneous Poisson process appears:

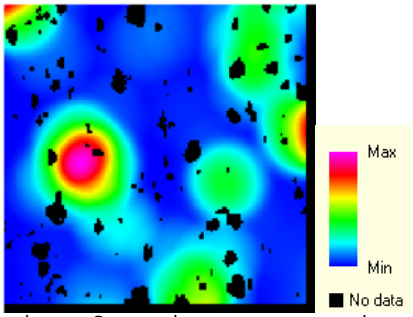


if you want to use the Epanečnikov kernel enable the check box "kernel", insert the radius R = 20 of the moving window (or the bandwidth R if you use the kernel estimator) and specify which data should be used for construction of the first-order intensity. Since you have only one pattern enable "Test only for pattern 1".
7) Press "Calculate index". Now *Programita* calculates the moving window estimate of the first-order intensity:



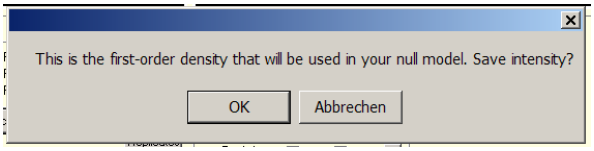
On the left the pattern data, on the right the estimated first-order intensity. The small black gaps are plants of other species which are excluded from the study area. This is the intensity estimate using the Epanečnikov kernel with bandwidth R= 20:

Note that it provides a somewhat smoother estimate of the intensity since cells further away are weighted lower, but the general pattern does not change. The bandwidth R has a much larger impact on the intensity function than the specific selection of the kernel.

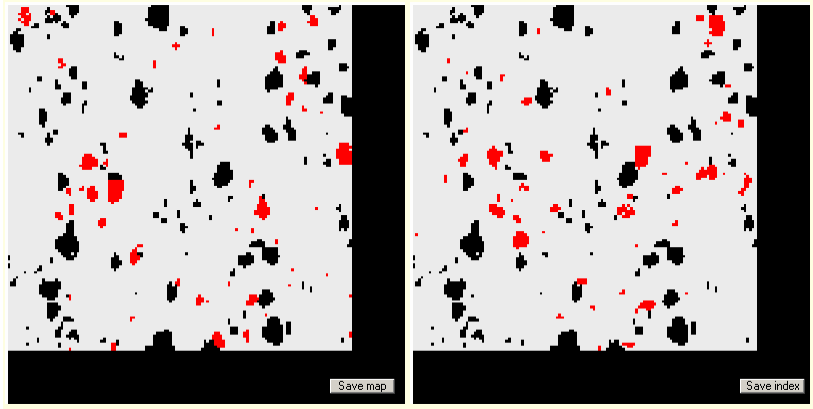


If you want to save the intensity function to use it in other analyses as plug-in file (see next example) select OK, otherwise select "Abbrechen". If you save the file, the name of the plug-in file will be int_name_R_r.int

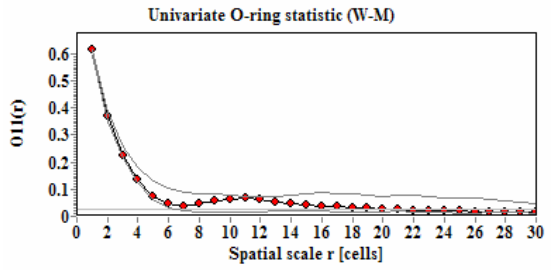
where "name" is the name of the data file (here m_ter_22), and r is the selected value for the radius of the moving window or bandwidth (here 20).



8) Programita now performs the simulations of the heterogeneous Poisson null model and shows you the pattern of the Monte Carlo null model on the right. The objects do not overlap the black "holes" made by the other species and are only distributed inside the smaller study region but more frequently in the pink and red areas of the intensity map.



9) After termination of the simulations of the null model a graph appears, showing the confidence limits of your null model (right). The slight clustering at scales r = 10, 11, and 12 visible after applying the CSR null model disappears with the heterogeneous Poisson null model:



Heterogeneous Poisson null model: plug-in intensity functions

(Example F_HP_2.res)

The heterogeneous Poisson null model uses the larger-scale intensity of the pattern for construction of the (first-order) intensity function to reveal the small-scale second-order characteristics of the pattern. In some cases, however, you may have additional information on variables that determine the environmental heterogeneity, e.g., elevation, or soil type. In this case *Programita* allows you to use a plug-in file containing the intensity function.

The plug-in a file has the extension *.int and the following design:

```
1 150 1 150  15573    1.0000
   1    1 1   0.857860
   1    2 1   0.799896
   1    3 1   0.749270

...

 130  129 1   0.074526
 130  130 1   0.079002
```

The first line contains, as usual, the information on the grid size: there are 150 cells in x-direction and 150 cells in y direction, the file contains information on a total of 15573 cells (if the study area has irregular shape cells outside the study area do not appear in the list) and the grid size is 1.000 (this information is for the point modus, in matrix modus it is always 1 since you cannot change the cell size).

The first column gives the x-coordinate, the second column the y-coordinate, the third column is always 1, and the fourth column gives the value of the intensity function at the given cell. Note that the intensity function must be scaled to a maximum value of 1 and should not have negative values.

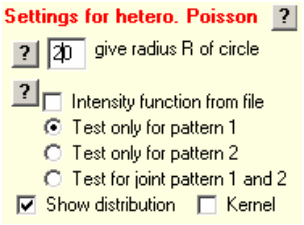
Be sure that the dimensions of the study rectangle and of the plug-in file match exactly!

This example is the same as the previous example, but a plug-in file is used to provide the intensity. Steps 1 - 5 are the same as in example F_HP_1.res.

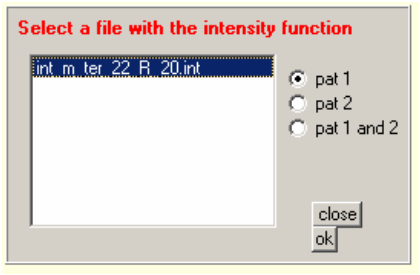
Input data file: m_ter_22.dat
How are your data organized: Matrix
Give modus of analysis Irregularly shaped study region
Which method will you use? Ring (or Circle)
Ring width: 1 (if intensity λ of cells is too low, select larger ring widths)
Set maximal radius rmax: 30 (too large scales slow down *Programita*)
Select modus of data: Data are given as matrix map
Give code numbers for pattern: Pattern 1: 1 1 1 1 (shrub species 1)
Pattern 2: 2 2 2 2 (code does not occur)
Mask: 22 11 -1 -1 (22: other shrubs, 11: outside strips)

---

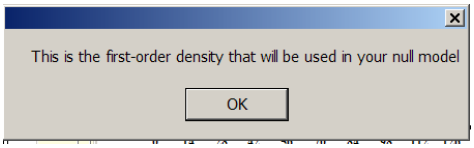
6) Enable the check box "Heterogeneous Poisson" in the null model window. A small settings window for the heterogeneous Poisson process appears:



to plug-in a file containing the intensity function enable the check-box "Intensity function from file" and a window with a list of all *.int plug-in files appears:



7) Select the file you wand to use (int_m_ter_22_R_20.int). Since you have only one pattern, enable "pat 1" (the intensity function is used for randomization of pattern 1) and press "ok". The intensity function appears on the right. Click OK in the message window



8) Press "Calculate index". Programita now performs the simulations of the heterogeneous Poisson null model and shows you the pattern of the Monte Carlo null model on the right.

Toroidal shift: Independence of bivariate patterns

The null model testing for independence of two point patterns assumes that two independent stochastic processes created the two component patterns (e.g., Goreaud & Pèlissier 2003). Departure from independence indicates that the two patterns display attraction or repulsion, regardless of the univariate pattern of either group by itself. Thus, the separate second-order structures of the patterns in their observed form has to be preserved, the dependence between the two patterns, however, has to be broken (Goreaud & Pèlissier 2003).

This can be achieved by simulations that involve random shifts of the whole of one component pattern relative to the other. The same idea applies for plants of finite size and irregular shape: pattern 1 remains fixed whereas pattern 2 is randomly shifted as a whole across the study area, using a torus (toroidal shift).

Note that this null model uses the torus method to treat plants that fall partly outside the study rectangle. For this reason no objects need to be defined and randomized (i.e., you do not need to enable real shape "Pat1" and/or "Pat2"), and the torus method requires that objects of different patterns are allowed to overlap. The latter may introduce a bias towards repulsion at small scales if the objects are known not to overlap. As an alternative, a univariate null model could be introduced to describe the second order structure of pattern 2 and, if appropriate, an overlap of plants could be prohibited.

Toroidal shift (Example F_In_1.res)

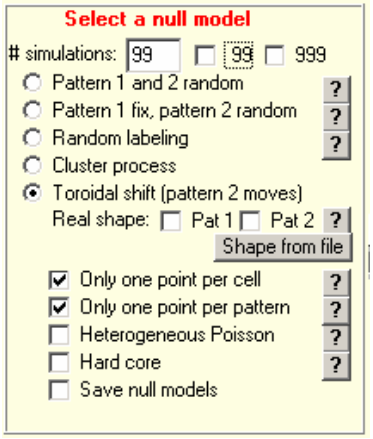
This example applies a heterogeneous Poison null model to the previous example.

Input data file: m_te22.dat
How are your data organized: Matrix
Give modus of analysis Analyze all data in rectangle
Which method will you use? Ring (or Circle)
Ring width: 1 (if intensity λ of cells is too low, select larger ring widths)
Set maximal radius rmax: 30 (too large scales slow down *Programita*)
Select modus of data: Data are given as matrix map
Give code numbers for pattern: Pattern 1: 1 1 1 1 (shrub species 1)
Pattern 2: 2 22 22 22 (other shrub species)

---

1) Click button "Calculate index". Your pattern appears on the left, and the *O*-ring function of your data appears on the right.

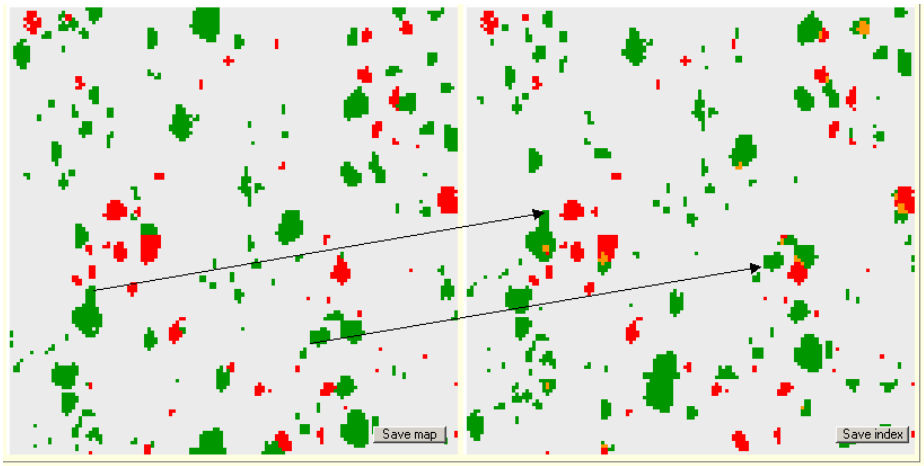
2) To determine Monte Carlo confidence limits for CSR, enable the check box "Calculate confidence limit" on the upper left. A window with settings for null models appears:



Select "Toroidal shift".

3) You can change the number of replicate simulations of the null model in the box "# simulations".

4) Press "Calculate index". Programita now performs the simulations of the Toroidal shift null model and shows you the pattern of the null model on the right. Note that the green pattern is shifted as indicated by the black arrows, and the objects may overlap (indicated by orange color).



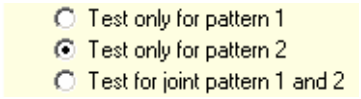
5) After termination of the simulations of the null model a graph appears, showing the confidence limits of your null model (right).

Antecedent condition: Randomising only pattern 2

The investigation of some processes, such as investigating facilitation or competition, is less concerned with independence but try to disprove instead that plants of one pattern are randomly distributed in the neighbourhood of the plants of the other pattern. Facilitation is indicated if plants of pattern 2 occur more frequently in the neighbourhood of plants of pattern 1 than expected under a random distribution of pattern 2 (or expected by the larger-scale intensity of pattern 2). Conversely, competition is indicated if they occur less frequently.

The appropriate bivariate null model for this question keeps the plants of pattern 1 fixed and distributes the plants of pattern 2 randomly over the area of the study area not occupied by plants of pattern 1 (called antecedent condition; Wiegand & Moloney 2004). Note that the null models "antecedent condition" and "independence" are not the same because "antecedent condition" does not preserve the observed second-order structure of pattern 2 and thus makes a specific assumption on the second-order structures of pattern 2. If plants of pattern 2 show large-scale variations in their intensity, one may distribute them in accordance to a heterogeneous Poisson null model which keeps the larger-scale intensity of the pattern (determined as kernel estimate, eq. HP1, HP2, and HP3) but destroys all second-order structures at smaller scales.

With a bivariate pattern you have different possibilities to randomize pattern 2 if you select a heterogeneous Poisson null model: you can use pattern 1, pattern 2 or the joined pattern 1 and 2 for construction of the first-order intensity used for distributing the objects of pattern 2. Which option is appropriate depends on your biological hypothesis.



If you want to investigate if there are small-scale second-order effects indicating competition or facilitation between plants of two different species you may use the first-order intensity of pattern 2 for randomization of plants of pattern 2. However, if you hypothesis is that the distribution of pattern 2 may depend on pattern 1 (e.g., if pattern 2 are seedlings and pattern 1 the parent trees) you may use the first-order intensity of pattern 1 for randomization of plants of pattern 2. Finally, if your hypothesis is that the two patterns follow the same environmental heterogeneity you may use the first-order intensity of the joined pattern for randomization of plants of pattern 2.

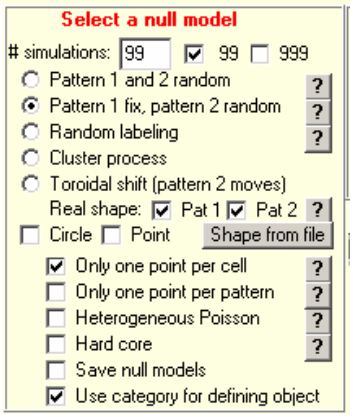
Antecedent condition (Example F_Ant_1.res)

This example applies a null model under antecedent condition to the previous example.

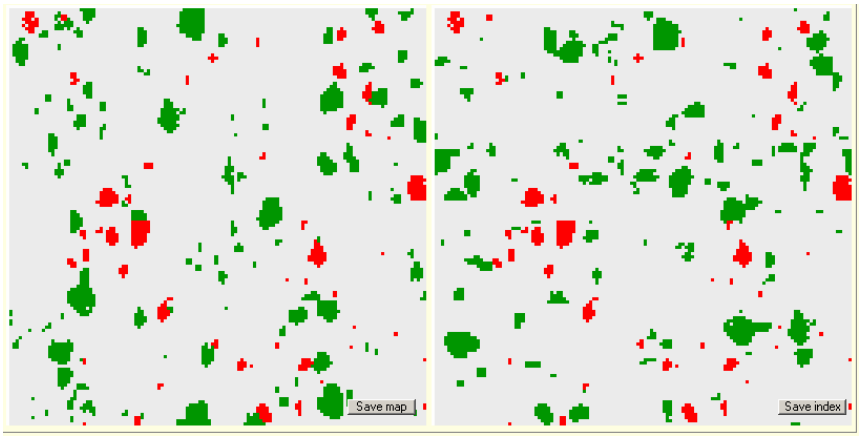
Input data file: m_te22.dat
How are your data organized: Matrix
Give modus of analysis Analyze all data in rectangle
Which method will you use? Ring (or Circle)
Ring width: 1 (if intensity λ of cells is too low, select larger ring widths)
Set maximal radius rmax: 30 (too large scales slow down *Programita*)
Select modus of data: Data are given as matrix map
Give code numbers for pattern: Pattern 1: 1 1 1 1 (shrub species 1)
Pattern 2: 22 2 2 2 (other shrub species)

---

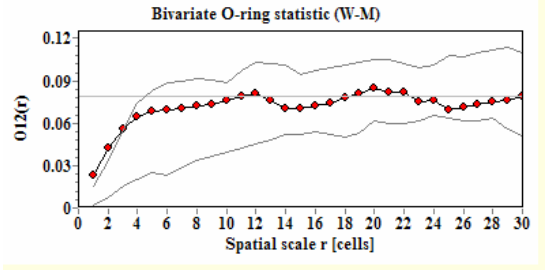
1) Click button "Calculate index". Your pattern appears on the left, and the *O*-ring function of your data appears on the right.
2) To determine Monte Carlo confidence limits for CSR, enable the check box "Calculate confidence limit" on the upper left. A window with settings for null models appears:



Select "Pattern 1 fix, pattern 2 random".
3) You can change the number of replicate simulations of the null model in the box "# simulations".
4) Press "Calculate index". Programita now performs the simulations of the null model and shows you the pattern of the null model on the right. Note that only the green pattern (= pattern 2) is randomized whereas the red pattern (= pattern 1) does not change:



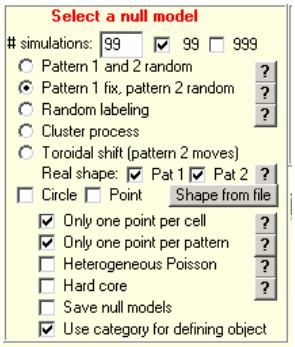
5) After termination of the simulations of the null model a graph appears, showing the confidence limits of your null model (right). There is a slight tendency to aggregation at small scales *r* = 1-3:since the objects in the data map (left map) touch more that the randomized objects (right map):



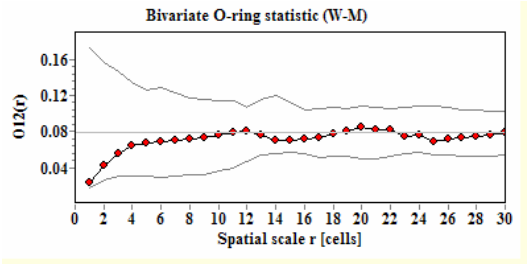
Antecedent condition (Example F_Ant_2.res)

This example repeats analysis of the previous example F_Ant_1.res, but allows overlap between objects of pattern 1 and pattern 2. Comparison between examples F_Ant_1.res and F_Ant_2.res demonstrates the difference such "small" difference in settings of the null model can make. Therefore you must carefully select the null model in accordance to the scientific question and knowledge on hand.

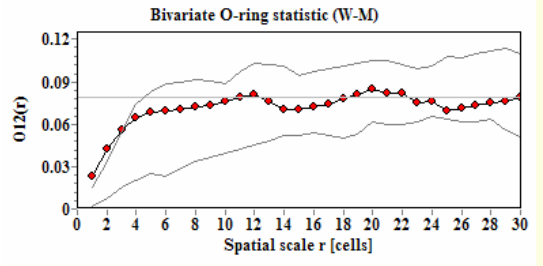
To allow overlap between pattern 1 and pattern 2 enable the check box "Only one point per pattern" in the null model window:



The departure from the null model observed in the previous example disappears:



Here for comparison the results without overlap. Note the stark differences in the confidence limits at smaller scales r < 10:



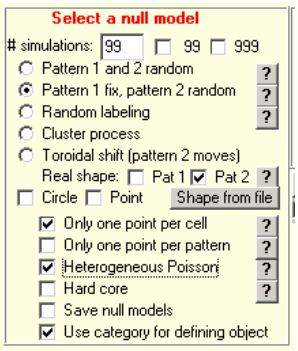
Antecedent condition (Example F_Ant_3.res)

This example applies a null model with antecedent condition to example F_Ant_1.res, but uses a heterogeneous Poisson null model for distribution of pattern 2 instead of CSR.

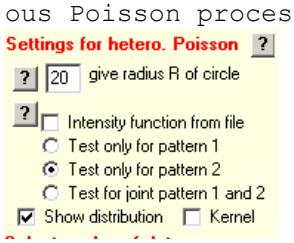
Input data file: m_te22.dat
How are your data organized: Matrix
Give modus of analysis Analyze all data in rectangle
Which method will you use? Ring (or Circle)
Ring width: 1 (if intensity λ of cells is too low, select larger ring widths)
Set maximal radius rmax: 30 (too large scales slow down *Programita*)
Select modus of data: Data are given as matrix map
Give code numbers for pattern: Pattern 1: 1 1 1 1 (shrub species 1)
Pattern 2: 22 2 2 2 (other shrubs)

---

1) Click button "Calculate index". Your pattern appears on the left, and the *O*-ring function of your data appears on the right.
2) To determine Monte Carlo confidence limits for CSR, enable the check box "Calculate confidence limit" on the upper left. A window with settings for null models appears:

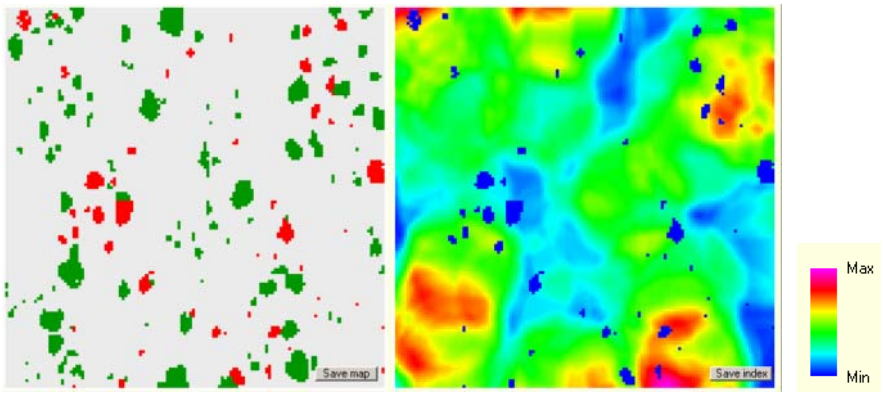


Select "Pattern 1 fix, pattern 2 random" and enable the check box "Pat 2" to consider objects of finite size and irregular shape for pattern 2. You do not need to enable "Pat 1" since pattern 1 is unchanged in this null model and does therefore not require definition of objects.
3) Enable the check box "Heterogeneous Poisson" in the null model window. A small settings window for the heterogeneous Poisson process appears:

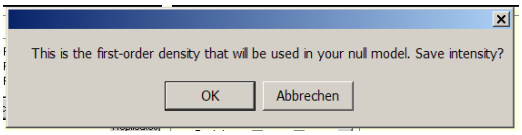


insert the radius R of the moving window (=20) and specify which data should be used for construction of the first-order intensity. With a bivariate pattern you have different possibilities: You can use pattern 1 ("Test only for pattern 1"), pattern 2 ("Test only for pattern 2") or pattern 1 and 2 ("Test for joined pattern 1 and 2") for construction of the first-order intensity used for distributing the objects of pattern 2. Which option is most appropriate depends on your biological hypothesis. In this example select "Test only for pattern 2".

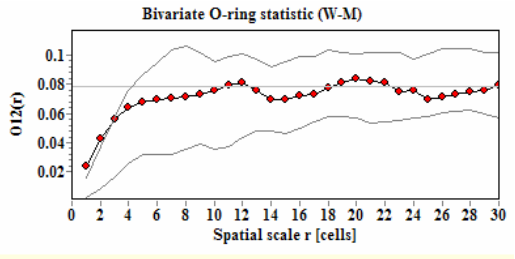
4) Press "Calculate index". Now *Programita* calculates the moving window estimate of the first-order intensity:



On the left Programita shows the pattern data, on the right the estimated first-order intensity. The blue holes are cells occupied by pattern 1. A message window appears:

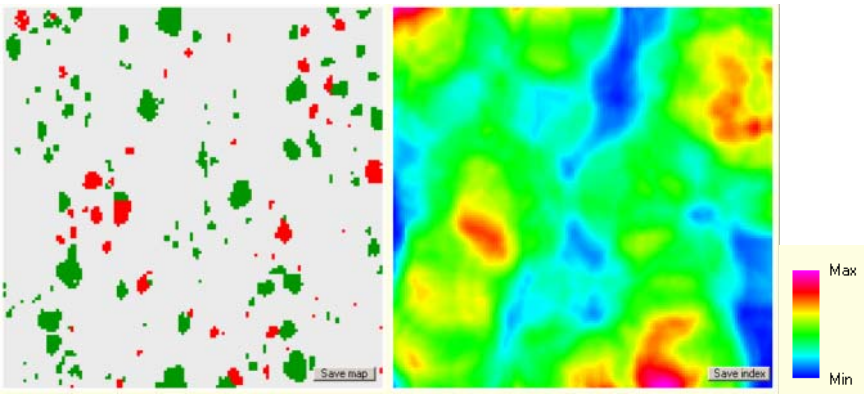


5) If you want to save the intensity function to use it in other analyses as plug-in file select OK, otherwise select "Abbrechen". If you save the file, the name of the plug-in file will be int_name_R_r.int where "name" is the name of the data file (here m_ter_22), and r is the selected value for the radius of the moving window or bandwidth (here 20).
6) Programita now performs the simulations of the heterogeneous Poisson null model and shows you the pattern of the Monte Carlo null model on the right.
7) After termination of the simulations of the null model a graph appears, showing the confidence limits of your null model (right).

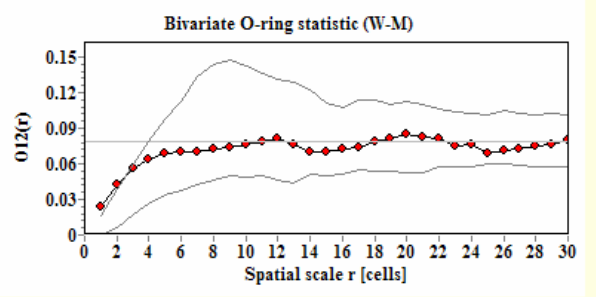


Antecedent condition (Example F_Ant_4.res)

To show the influence of the selection of the pattern for definition of the first order intensity we repeat the previous example (F_Ant_3.res), but use the data of pattern 1 and pattern 2 for construction if the first-order intensity.



Compare the difference of the first-order intensity to the previous example! However, since both pattern 1 and pattern 2 follow CSR, there is no difference in the result to the previous example:



Random labelling

Random labelling is the appropriate null model for a null hypothesis corresponding to the absence of interaction between the two types of points if the points of both patterns were created by one process (e.g., trees), but a subsequent process created the labels "pattern 1" (= surviving trees) and "pattern 2" (= dead trees) (Goreaud & Pèlissier 2003). The null model of random labelling then assumes that the process which assigned label to plants was a random process. In a wider sense, random labelling is an appropriate null model to test the null hypothesis that the labels do not show any spatial structure.

An important ingredient of testing for random labelling is the invariance of *g*- and *K*-functions under random thinning (i.e., randomly removing points does not change the second-order properties of uni- or bivariate patterns). Thus, $g_{11}(r) = g_{22}(r) = g_{12}(r) = g_{21}(r)$. This property suggests different test statistics to test different aspects of random labelling:

- univariate random labeling uses $g_{11}(r)$ as test statistic,
- conventional bivariate random labeling uses $g_{12}(r)$ as test statistic (Goreaud & Pèlissier 2003),
- the differences $g_{22}(r)$ - $g_{11}(r)$ which tests if pattern 2 is more clustered than pattern 1,
- the difference $g_{12}(r)$ - $g_{11}(r)$ which evaluates if there are (relatively) more type 2 points than type 1 points in rings (circles) of radius r around type 1 points.

Random labelling for objects of finite size can be performed in analogy to random labelling of point patterns: here one needs to randomly assign case labels to n_1 of the $n_1 + n_2$ objects of the joined pattern.

However, the finite size of objects may introduce violation of the assumption of random thinning if the number of plants is small and the size class distribution of the two patterns is not approximately the same. Therefore care is required by interpreting the results of random labelling for objects of finite size and irregular shape. Departures from random labelling may stem from differences in the number of objects in pattern 1 and pattern 2 and the size structure of the two patterns.

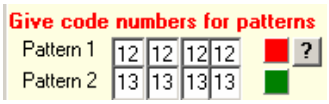
Random labeling (Example RL_1.res)

In this example we hypothesize that the labels pattern 1 and pattern 2 of objects of a bivariate pattern are randomly distributed and apply the random labeling null model. To test the random labeling hypothesis more comprehensibly we use several test statistics.

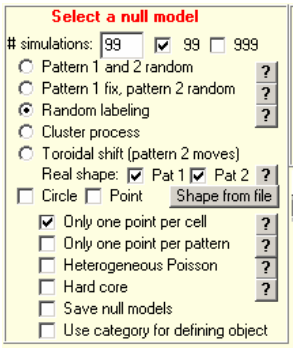
Input data file: Figure2.asc
How are your data organized: Matrix
Give modus of analysis Analyze all data in rectangle
Which method will you use? Ring (or Circle)
Ring width: 1 (if intensity λ of cells is too low, select larger ring widths)
Set maximal radius rmax: 30 (too large scales slow down *Programita*)
Select modus of data: Data are given as matrix map
Give code numbers for pattern: Pattern 1: 13 13 13 13 (shrub species 1)
Pattern 2: 12 12 12 12 (shrub species 2)

---

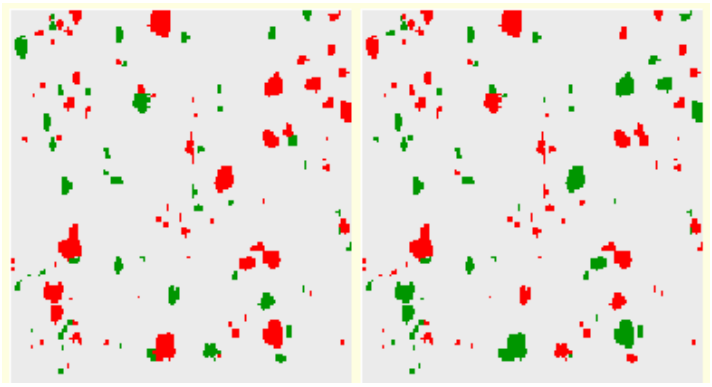
1) highlight the data file "Figure2.asc" in window **Input data file.**
2) select "Matrix" in **How are your data organized**
3) select "Analyze all data in rectangle" **in Give modus of analysis**
4) select "Data are given as matrix map" in **Select modus of data**
5) select the code numbers for pattern 1 and pattern 2 in **Give code numbers for patterns**: write 12 in all windows reserved for pattern 1 (the first shrub species) and write 13 in all windows reserved for pattern 2 (the second shrub species).



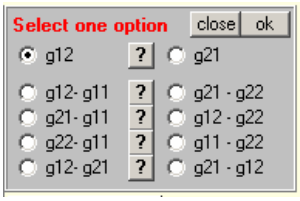
6) enable the check box "Calculate confidence limit" on the upper left. A window with settings for null models appears. Enable the check boxes "Pat 1" and "Pat 2" and select "Random labeling":



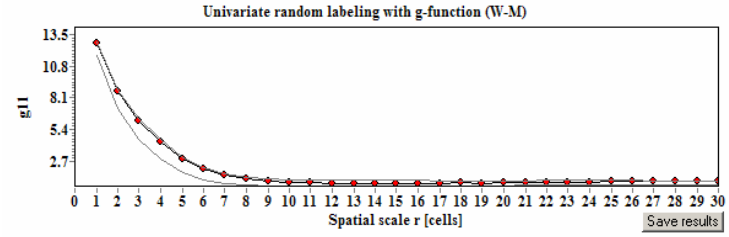
7) click "Calculate index". *Programita* now performs the simulations of the random labeling null model and shows you the pattern of the null model on the right. Note that the cells occupied by pattern 1 or pattern 2 are exactly the same, but the color (= pattern 1 or pattern 2) changes:



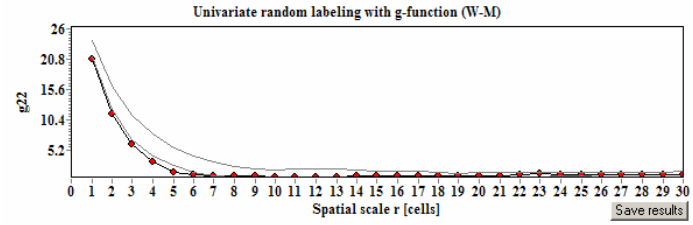
8) After termination of the simulations a window appears:



9) Enable first g12 to test for univariate random labeling. *Programita* shows the univariate *g*11-function (instead of the *O*-ring statistic) together with the confidence limits for the univariate random labeling null model:

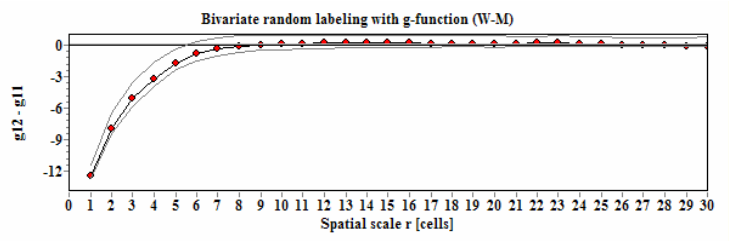

Univariate random labeling with g-function (W-M)
g11
13.5
10.8
8.1
5.4
2.7
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
Spatial scale r [cells]
Save results

The results show that the cases (pattern 1) have the same second-order structure than the joined pattern of case and control; although there is a non-significant tendency to be more clustered at scales r < 10. Interestingly, exchanging case and controls (i.e., enabling g21) yields a different results:

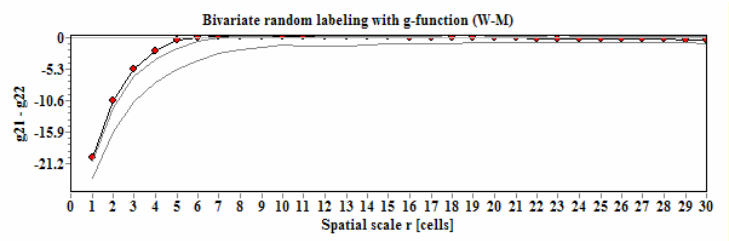

Univariate random labeling with g-function (W-M)
g22
26
20.8
15.6
10.4
5.2
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
Spatial scale r [cells]
Save results

for scales r = 1- 7, pattern 2 is significantly less clustered than the joined pattern.

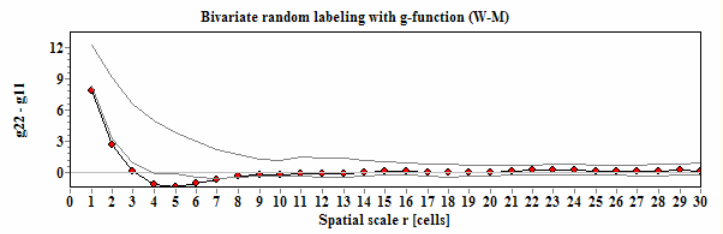
10) Using the test statistic g12 - g11 shows that cells of pattern 2 surround cells of pattern 1 as cells of pattern 1:



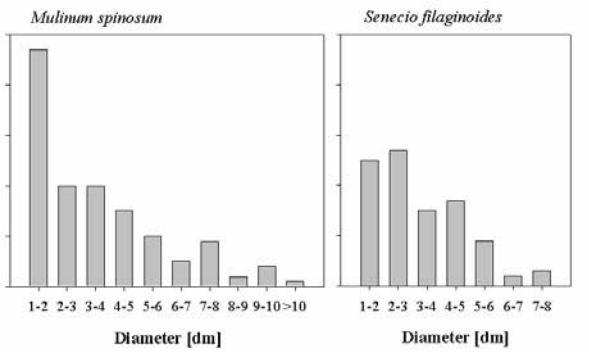
11) However, the test with the test inverse statistic g21 - g22 shows that cells of pattern 1 surround cells of pattern 2 at scales r = 1 - 7 less than cells of pattern 2:



12) Finally, the test statistic g22 - g11 shows that pattern 2 is at scales r = 1 - 7 less clustered than pattern 1:



Since the departures from random labeling occurred for small scales r < 8 which are within the radius of the shrubs, they may be due to slight differences in the size distribution of pattern 1 and pattern 2. Indeed, *Mulinum* shrubs (code 12) are at scales *r* = 1 - 7 (dm) larger than *Senecio* shrubs (code 13):



This illustrates that the interpretation of the results of random labeling of objects with finite site and irregular shape has to be done with care.

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